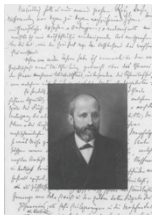
National Human Genome Research Institute Division of Intramural Research

The Genomic Landscape: *circa* 2010

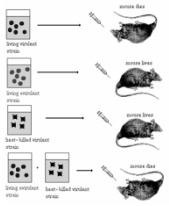
Eric Green, M.D., Ph.D.
Director, NHGRI

Foundational Milestones in Genetics & Genomics

Mendel ***1865***

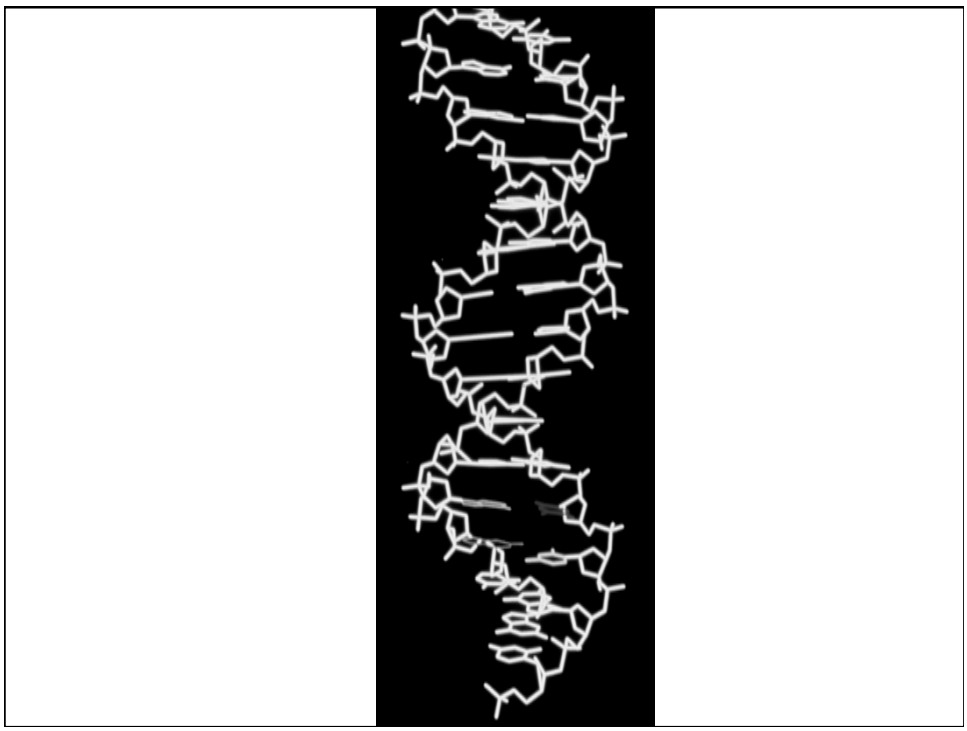


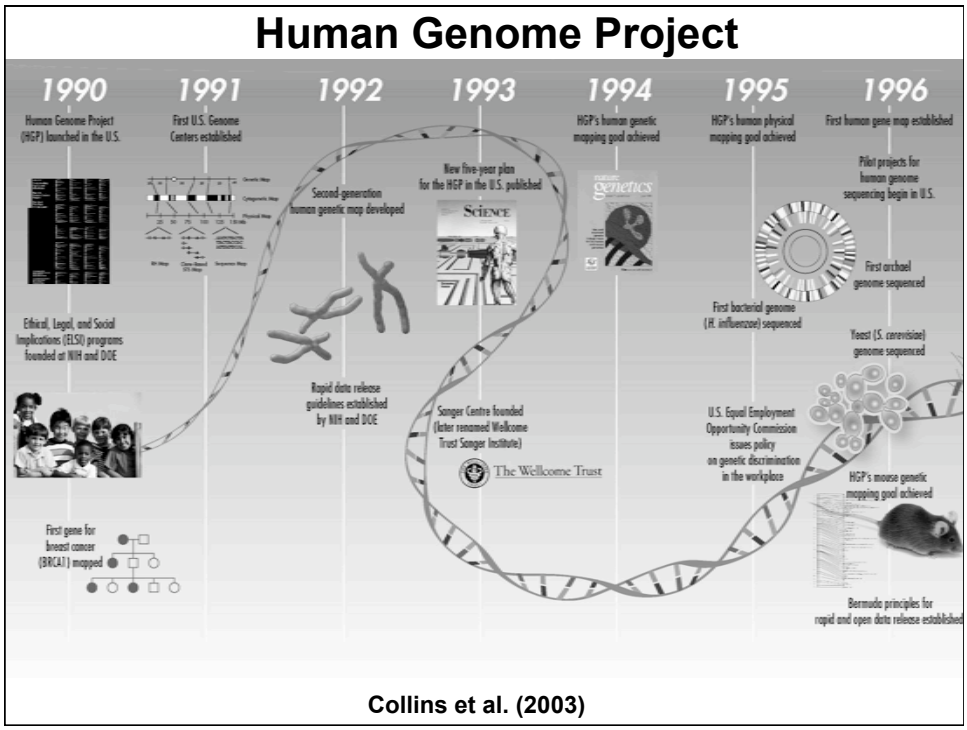
Miescher ***1871***



Avery ***1944***

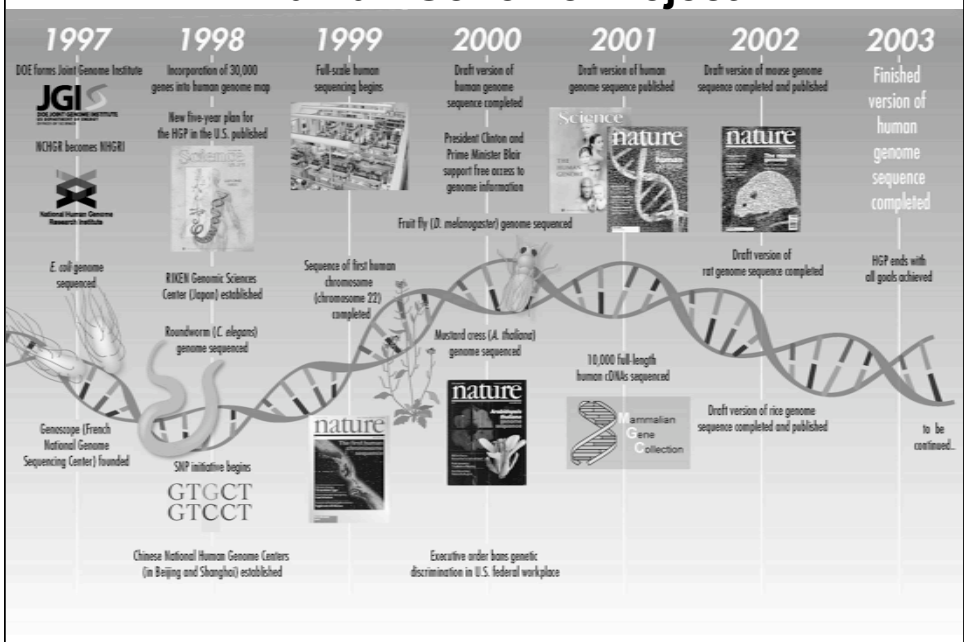
Watson & Crick ***1953***





Collins et al. (2003)

Human Genome Project



Collins et al. (2003)

Outline

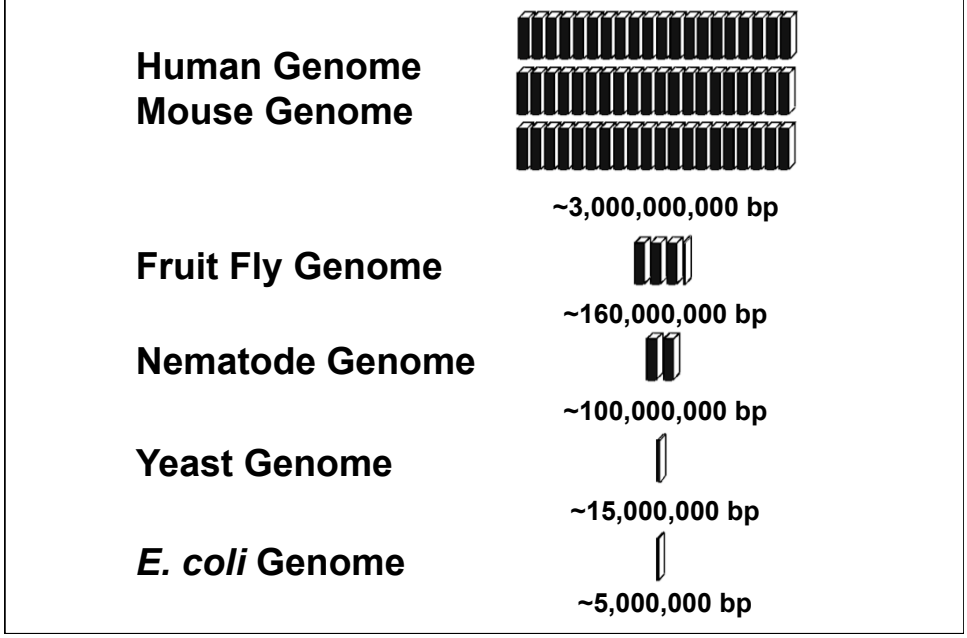
I. Fundamentals of Genome Mapping & Sequencing

II. Mapping & Sequencing in the Human Genome Project

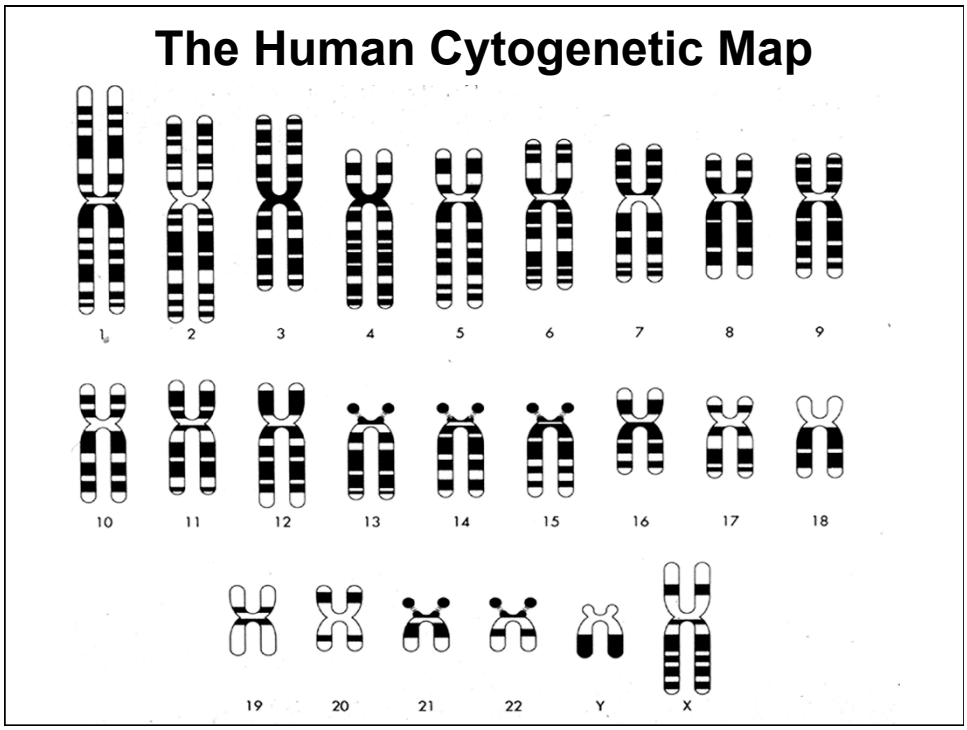
III. Comparative Sequencing

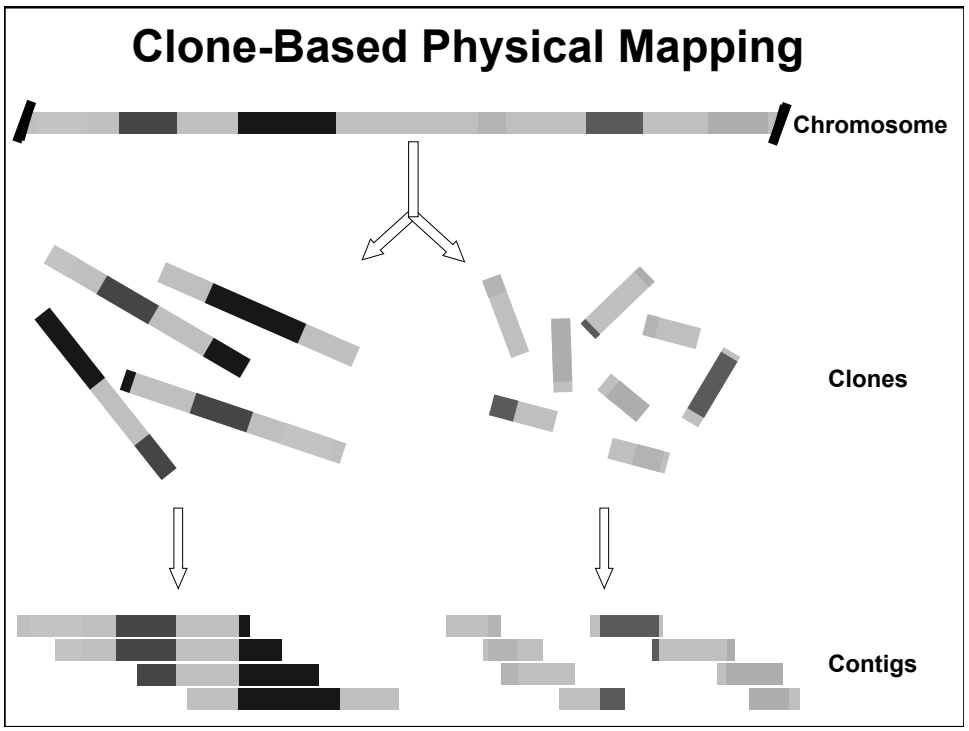
IV. New Frontiers in Genomics

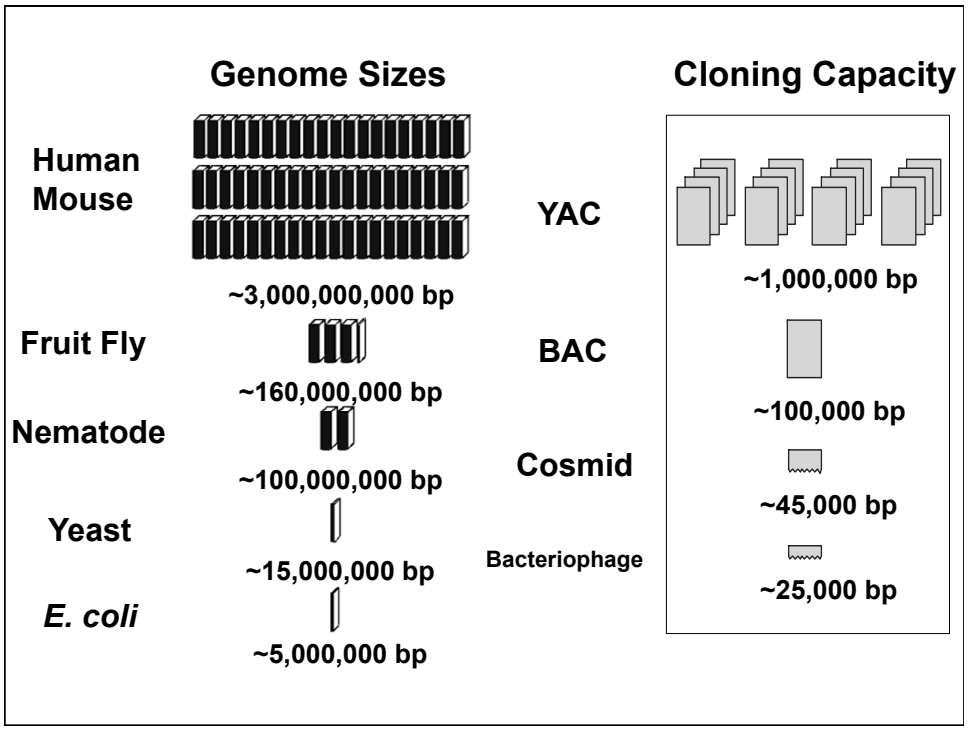
Genome Sizes

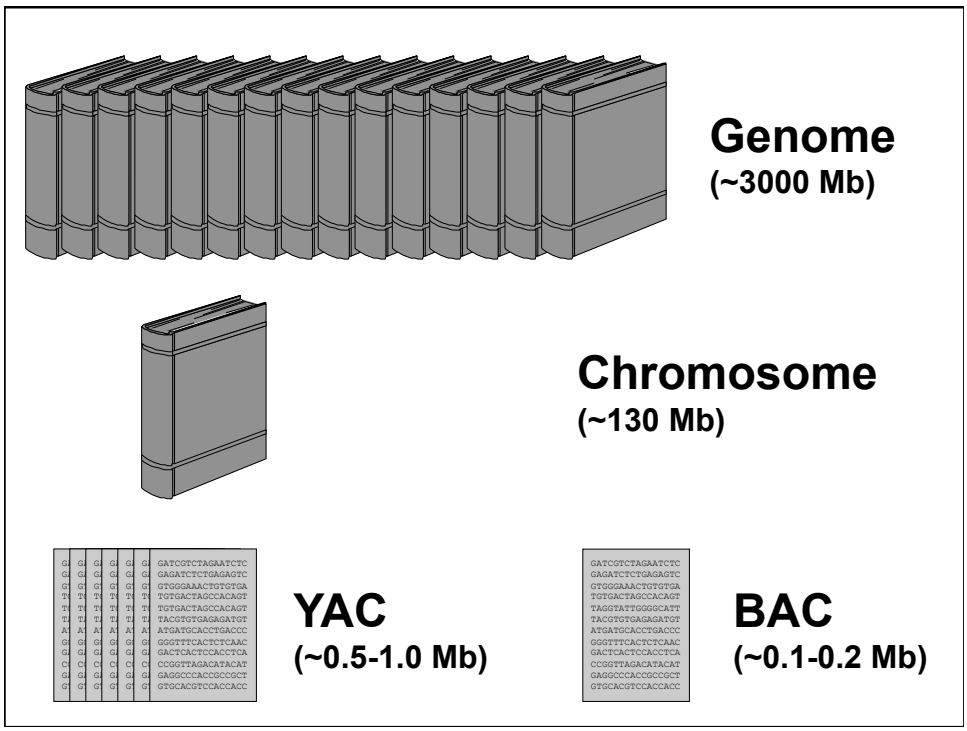


The Human Cytogenetic Map




Clone-Based Physical Mapping
Chromosome
Clones
Contigs


Genome Sizes
Cloning Capacity
Human
Mouse
~3,000,000,000 bp
Fruit Fly
~160,000,000 bp
Nematode
~100,000,000 bp
Yeast
~15,000,000 bp
E. coli
~5,000,000 bp
YAC
~1,000,000 bp
BAC
~100,000 bp
Cosmid
~45,000 bp
Bacteriophage
~25,000 bp


Genome
(~3000 Mb)
Chromosome
(~130 Mb)
GATCGTCTAGAATCTC
GAGATCTCTGAGAGTC
GTGGGAAACTGTGTGA
TGTGACTAGCCACAGT
TGTGACTAGCCACAGT
TACGTGTGAGAGATGT
ATGATGCACCTGACCC
GGGTTTCACTCTCAAC
GACTCACTCCACCTCA
CCGGTTAGACATACAT
GAGGCCCACCGCCGCT
GTGCACGTCCACCACC
YAC
(~0.5-1.0 Mb)
GATCGTCTAGAATCTC
GAGATCTCTGAGAGTC
GTGGGAAACTGTGTGA
TGTGACTAGCCACAGT
TAGGTATTGGGGCATT
TACGTGTGAGAGATGT
ATGATGCACCTGACCC
GGGTTTCACTCTCAAC
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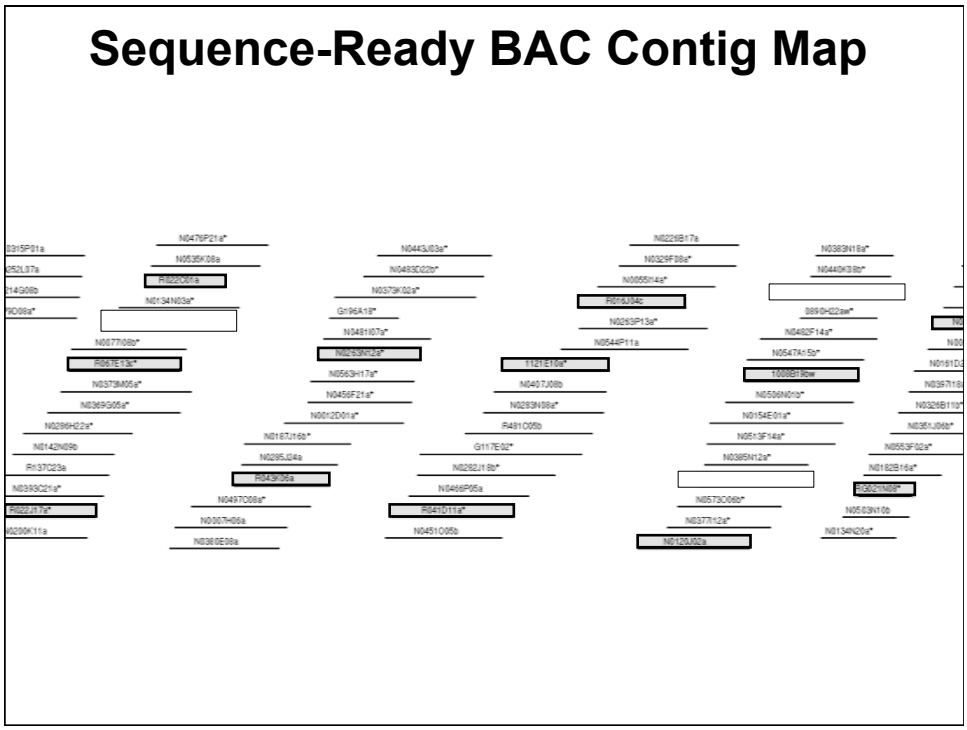
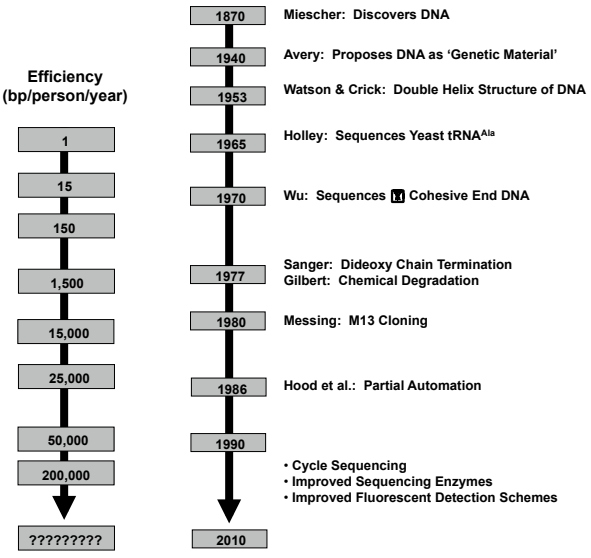
GAGGCCCACCGCCGCT
GTGCACGTCCACCACC
BAC
(~0.1-0.2 Mb)

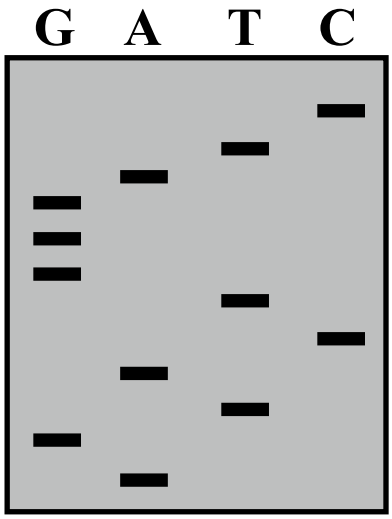

Sequence-Ready BAC Contig Map

DNA Sequencing

History of DNA Sequencing

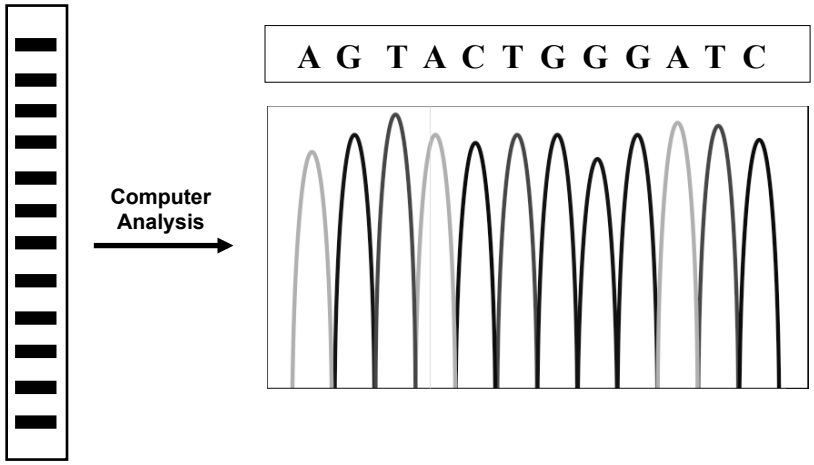


DNA Tagged with Radioactivity

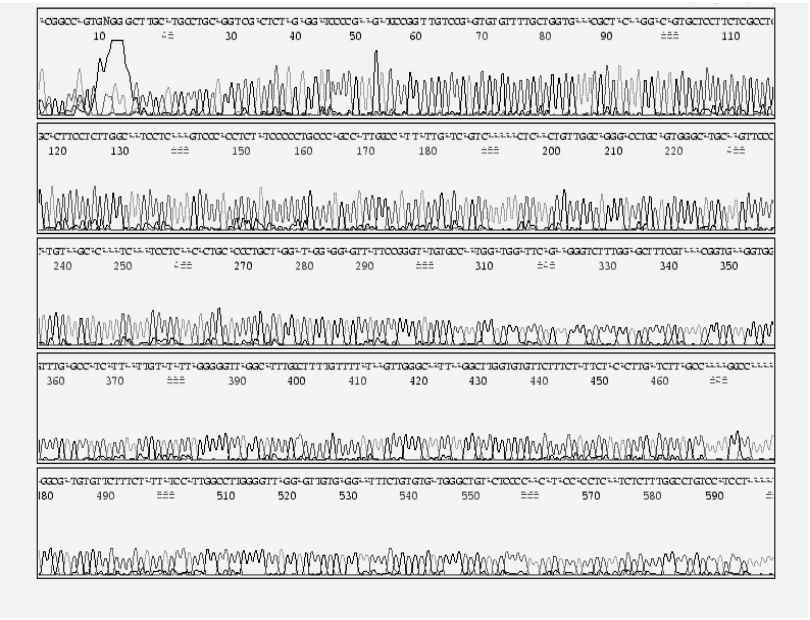


G: G Reaction
A: A Reaction
T: T Reaction
C: C Reaction

Analyzing Fluorescent DNA Sequencing Data



Fluorescent DNA Sequencing Results

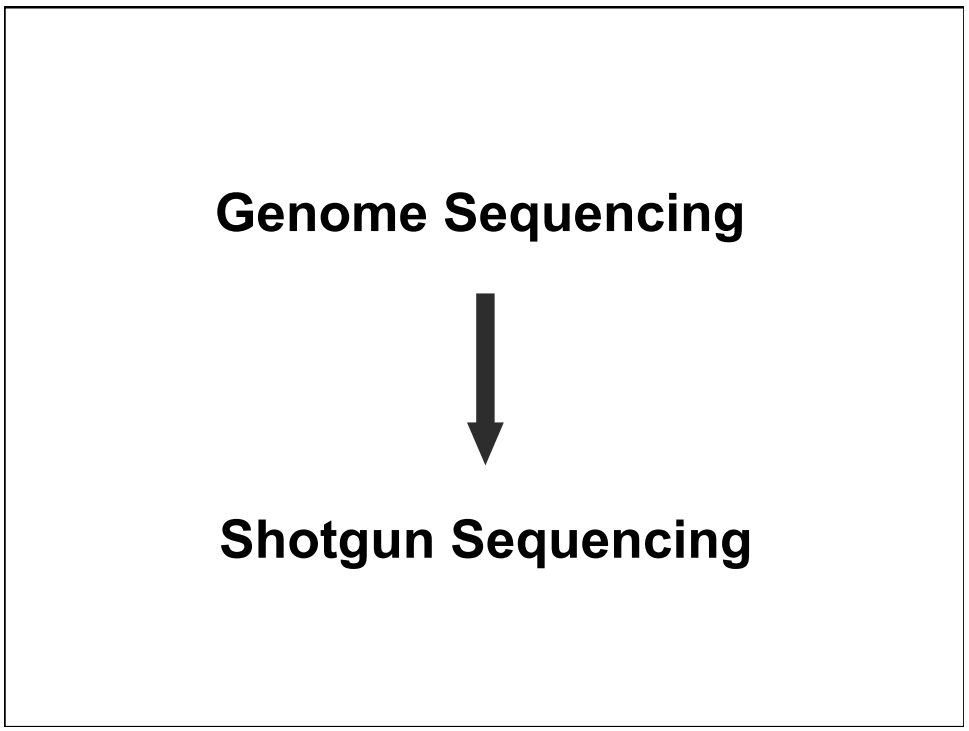


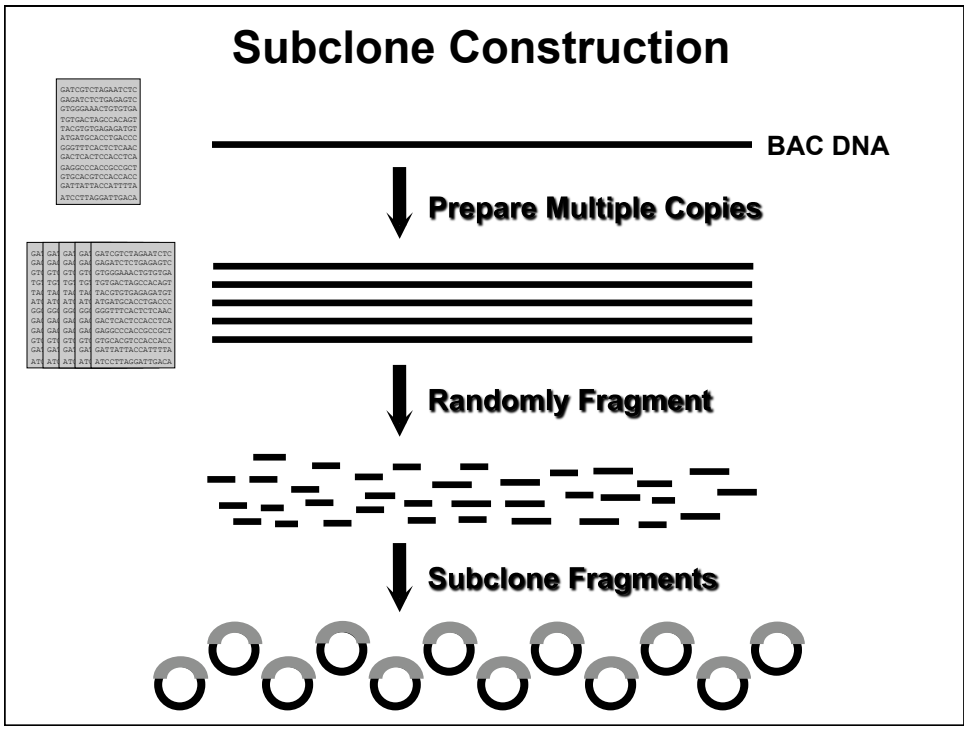
Analysis of Gene Expression

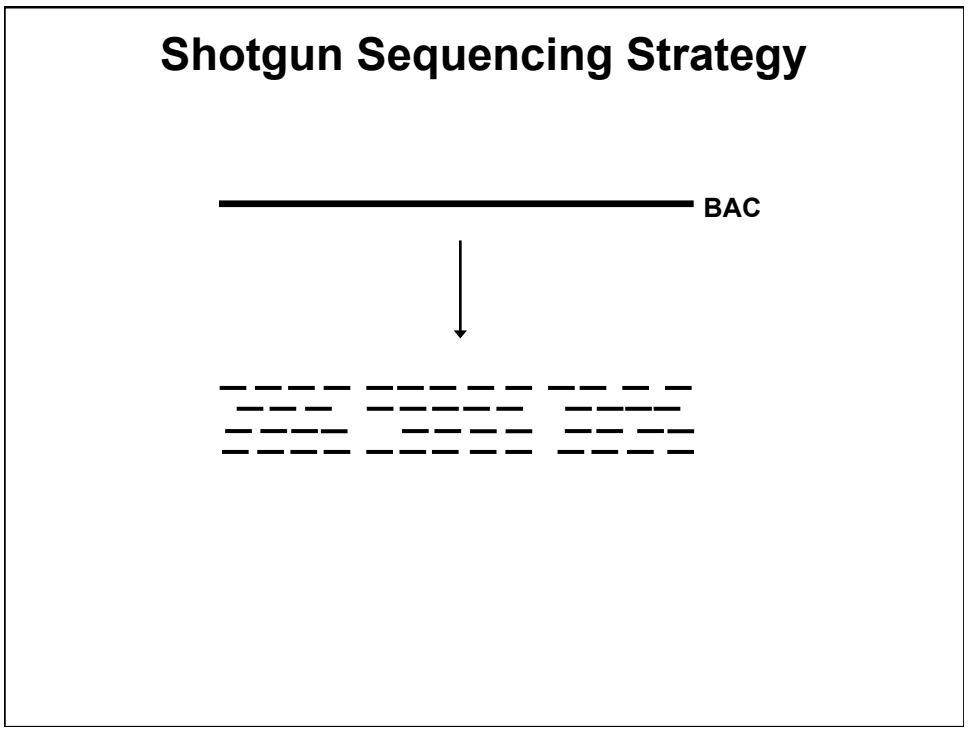
- **ESTs: Expressed-Sequence Tags**
- **SAGE: Serial Analysis of Gene Expression**
- **Full-Insert (Full-Length) cDNA Sequencing**

Mammalian Gene Collection

mgc.nci.nih.gov


Genome Sequencing
Shotgun Sequencing


Subclone Construction
BAC DNA
Prepare Multiple Copies
Randomly Fragment
Subclone Fragments



Poisson Calculations

The sequencing strategy for the shotgun approach follows the Lander and Waterman application of the Poisson distribution

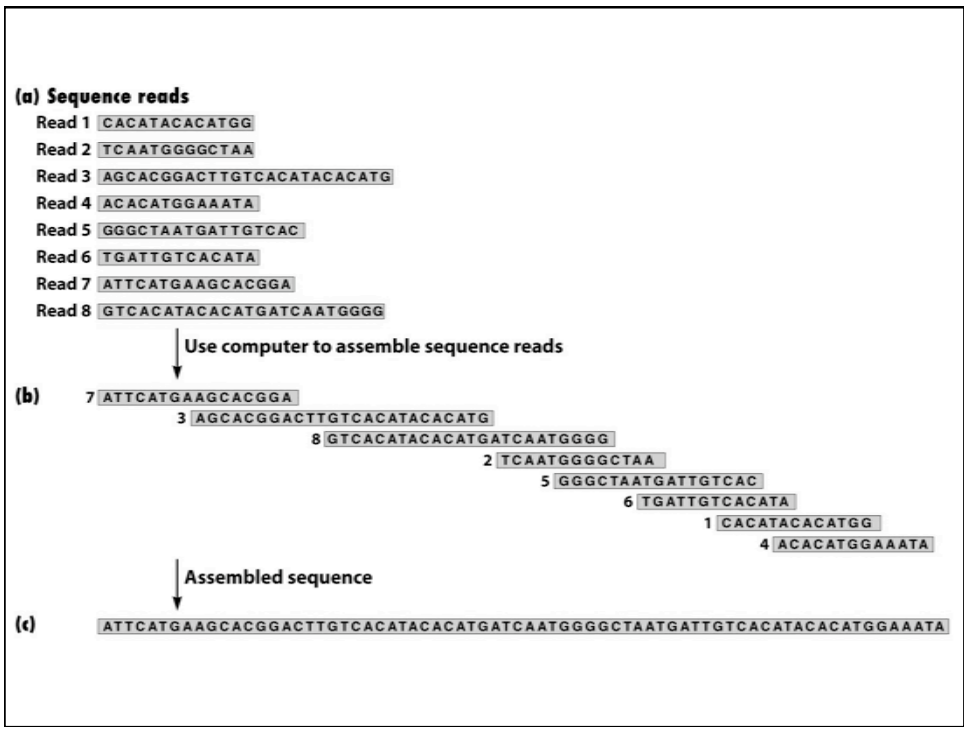
The probability a base is not sequenced is given by:

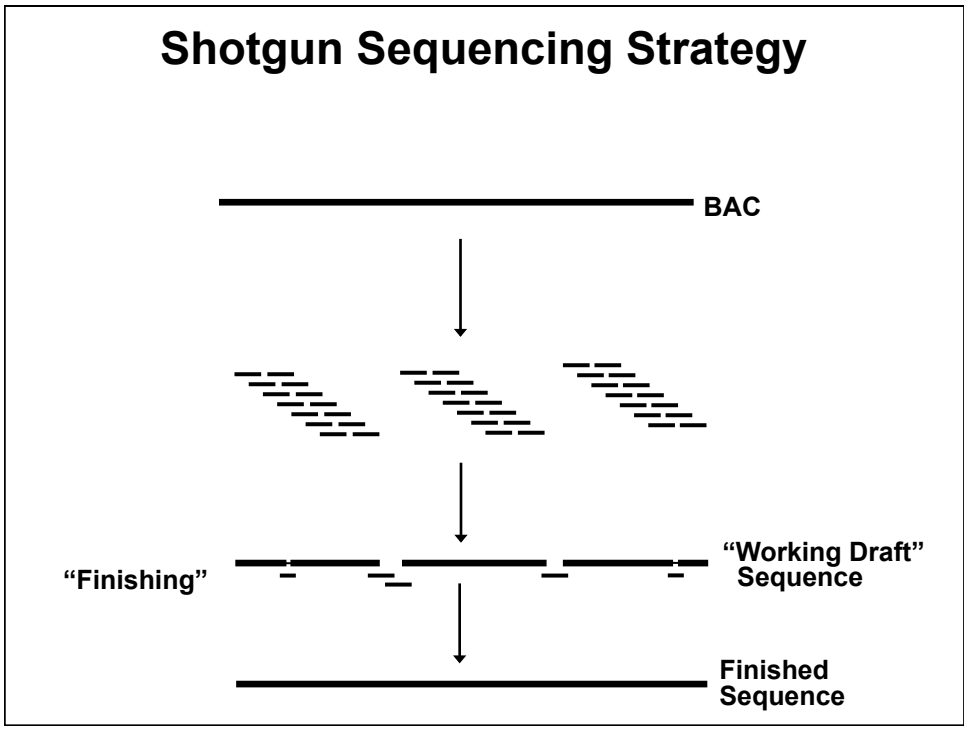
$$P_0 = e^{-c}$$

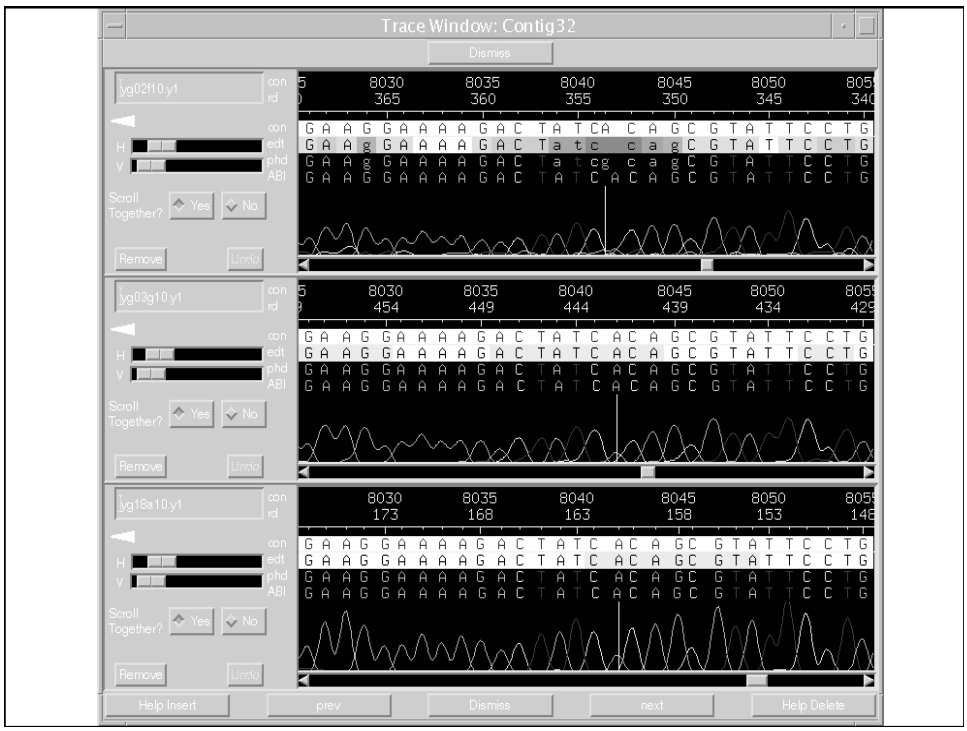
Where:

- c = fold sequence coverage (c=LN/G),
- LN = # bases sequenced, i.e. L = average sequencing read length and N = # reads
- G = target sequence length
- e = 2.718 (e=2.718281828459)

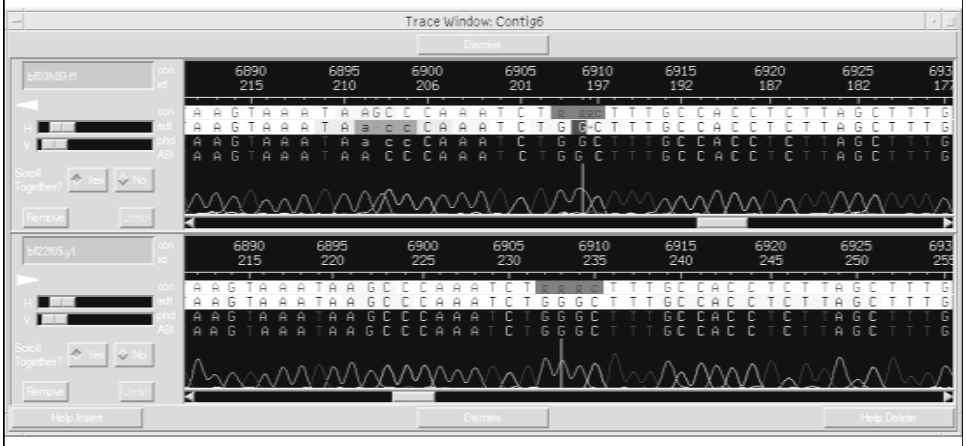
Fold Coverage	$P_0=e^{-c}$	% not sequenced	% sequenced
1	0.37	37%	63%
2	0.135	13.5%	87.5%
3	0.05	5%	95%
4	0.018	1.8%	98.2%
5	0.0067	0.6%	99.4%
6	0.0025	0.25%	99.75%
7	0.0009	0.09%	99.91%
8	0.0003	0.03%	99.97
9	0.0001	0.01%	99.99%
10	0.000045	0.005%	99.995%


(a) Sequence reads
Read 1 CACATACACATGG
Read 2 TCAATGGGGCTAA
Read 3 AGCACGGACTTGTCACATACACATG
Read 4 ACACATGGAAATA
Read 5 GGGCTAATGATTGTCAC
Read 6 TGATTGTCACATA
Read 7 ATTCATGAAGCACGGA
Read 8 GTCACATACACATGATCAATGGGG
Use computer to assemble sequence reads
(b)
7 ATTCATGAAGCACGGA
3 AGCACGGACTTGTCACATACACATG
8 GTCACATACACATGATCAATGGGG
2 TCAATGGGGCTAA
5 GGGCTAATGATTGTCAC
6 TGATTGTCACATA
1 CACATACACATGG
4 ACACATGGAAATA
Assembled sequence
(c)
ATTCATGAAGCACGGACTTGTCACATACACATGATCAATGGGGCTAATGATTGTCACATACACATGGAAATA


Shotgun Sequencing Strategy
BAC
"Finishing"
"Working Draft" Sequence
Finished Sequence



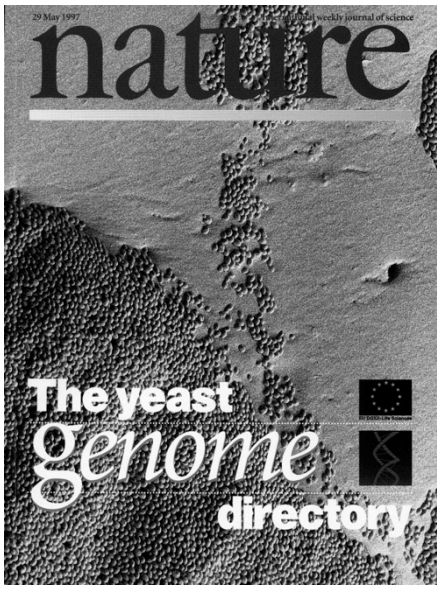
Sequence Finishing: Resolving Ambiguities



***** Sequence Finishing: Remains Relatively Expensive *****

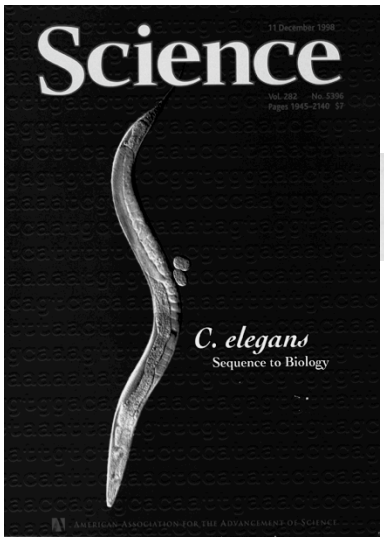
Historically Significant Genome Sequencing Projects

First Eukaryotic Genome Sequence



Goffeau et al. (1997)

First Animal Genome Sequence

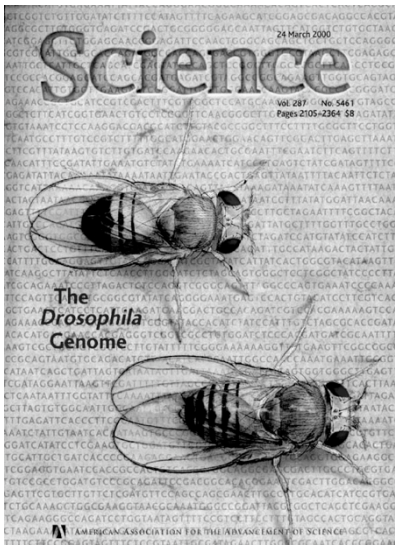


Genome Sequence of the Nematode *C. elegans*: A Platform for Investigating Biology

The *C. elegans* Sequencing Consortium*

***C. elegans* Sequencing Consortium (1998)**

Second Animal Genome Sequence



THE *DROSOPHILA* GENOME

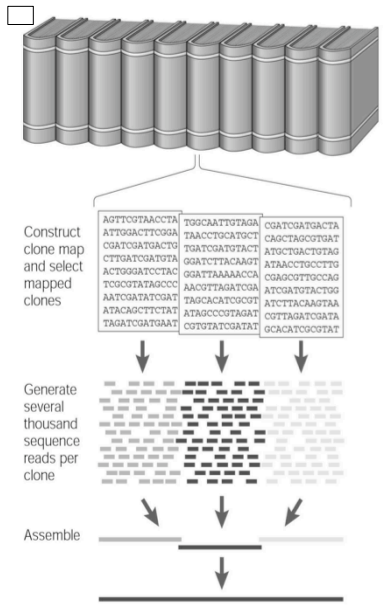
REVIEW

The Genome Sequence of *Drosophila melanogaster*

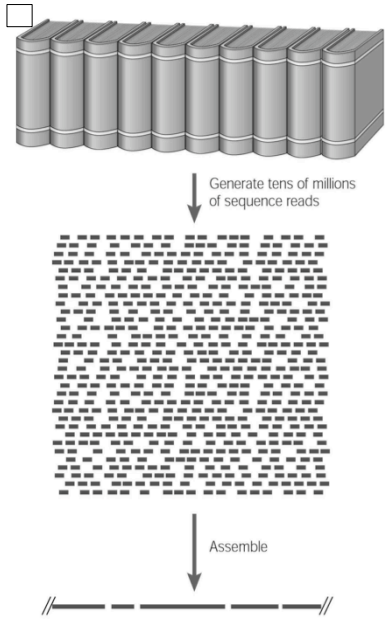
Mark D. Adams,[1*] Susan E. Celniker,[2] Robert A. Holt,[1] Cheryl A. Evans,[1] Jeannine D. Gocayne,[1] Peter G. Amanatides,[1] Steven E. Scherer,[3] Peter W. Li,[1] Roger A. Hoskins,[2] Richard F. Galle,[2] Reed A. George,[2] Suzanna E. Lewis,[4] Stephen Richards,[4] Michael Ashburner,[5] Scott N. Henderson,[1] Granger G. Sutton,[1] Jennifer R. Wortman,[1] Mark D. Yandell,[1] Qing Zhang,[1] Lin X. Chen,[1] Rhonda C. Brandon,[1] Yu-Hui C. Rogers,[1] Robert G. Blazej,[2] Mark Champe,[2] Barret D. Pfeiffer,[2] Kenneth H. Wan,[2] Clare Doyle,[2] Evan G. Baxter,[2] Gregg Helt,[4] Catherine R. Nelson,[4] George L. Gabor Miklos,[2] Josep F. Abril,[6] Anna Agbayani,[2] Hui-Jin An,[1] Cynthia Andrews-Pfannkoch,[1] Danita Baldwin,[1] Richard M. Ballew,[1] Anand Basu,[1] James Baxendale,[1] Leyla Bayraktaroglu,[3] Ellen M. Beasley,[1] Karen Y. Beeson,[1] P. V. Benos,[10] Benjamin P. Berman,[2] Deepali Bhandari,[1] Slava Bolshakov,[11] Dana Borkova,[12] Michael R. Botchan,[13] John Bouck,[2] Peter Brokstein,[4] Phillipe Brottier,[14] Kenneth C. Burtis,[15] Dana A. Busam,[1] Heather Butler,[16] Edouard Cadieu,[17] Angela Center,[1] Ishwar Chandra,[1] J. Michael Cherry,[18] Simon Cawley,[19] Carl Dahlke,[1] Lionel B. Davenport,[1] Peter Davies,[1] Beatriz de Pablos,[20] Arthur Delcher,[1] Zuoming Deng,[1] Anne Deslattes Mays,[1] Ian Dew,[1] Suzanne M. Dietz,[1] Kristina Dodson,[1] Lisa E. Doup,[1] Michael Downes,[21] Shannon Dugan-Rocha,[3] Boris C. Dunkov,[22] Patrick Dunn,[1] Kenneth J. Durbin,[3] Carlos C. Evangelista,[1] Concepcion Ferraz,[23] Steven Ferriera,[1] Wolfgang Fleischmann,[5] Carl Fosler,[1] Andrei E. Gabrielian,[1] Neha S. Garg,[1] William M. Gelbart,[9] Ken Glasser,[1] Anna Glodek,[1] Fangcheng Gong,[1] J. Harley Gorrell,[2] Zhiping Gu,[1] Ping Guan,[1] Michael Harris,[1] Nomi L. Harris,[2] Damon Harvey,[4] Thomas J. Heiman,[1] Judith R. Hernandez,[3] Jarrett Houck,[1] Damon Hostin,[1] Kathryn A. Houston,[2] Timothy J. Howland,[1] Ming-Hui Wei,[1] Chinyere Ibegwam,[1] Mena Jalali,[1] Francis Kalush,[1] Gary H. Karpen,[21] Zhaoxi Ke,[1] James A. Kennison,[24] Karen A. Ketchum,[1] Bruce E. Kimmel,[2] Chinnappa D. Kodira,[1] Cheryl Kraft,[1] Saul Kravitz,[1] David Kulp,[4] Zhongwu Lai,[1] Paul Lasko,[25] Yiding Lei,[1] Alexander A. Levitsky,[1] Jiayin Li,[1] Zhenya Li,[1] Yong Liang,[1] Xiaoying Lin,[26] Xiangjun Liu,[1] Bettina Mattei,[1] Tina C. McIntosh,[1] Michael P. McLeod,[3] Duncan McPherson,[1] Gennady Merkulov,[1] Natalia V. Milshina,[1] Clark Mobarry,[1] Joe Morris,[4] Ali Moshrefi,[2] Stephen M. Mount,[27] Mee Moy,[1] Brian Murphy,[1] Lee Murphy,[28] Donna M. Muzny,[3] David L. Nelson,[3] David R. Nelson,[29] Keith A. Nelson,[1] Katherine Nixon,[2] Deborah R. Nusskern,[1] Joanne M. Pacleb,[2] Michael Palazzolo,[2] Gjange S. Pittman,[1] Sue Pan,[1] John Pollard,[1] Vinita Puri,[1] Martin G. Reese,[4] Knut Reinert,[1] Karin Remington,[1] Robert D. C. Saunders,[30] Frederick Scheeler,[1] Hua Shen,[3] Bixiang Christopher Shue,[1] Inga Sidén-Kiamos,[31] Michael Simpson,[1] Marian P. Skupski,[1] Tom Smith,[1] Eugene Spier,[1] Allan C. Spradling,[31] Mark Stapleton,[2] Renee Strong,[1] Eric Sun,[1] Robert Svirskas,[32] Cyndee Tector,[1] Russell Turner,[1] Eli Venter,[1] Aihui H. Wang,[1] Xin Wang,[1] Zhen-Yuan Wang,[1] David A. Wassarman,[33] George M. Weinstock,[3] Jean Weissenbach,[14] Sherita M. Williams,[1] Trevor Woodage,[1] Kim C. Worley,[3] David Wu,[1] Song Yang,[2] Q. Alison Yao,[1] Jane Ye,[1] Ru-Fang Yeh,[10] Jayshree S. Zaveri,[1] Ming Zhan,[1] Guangren Zhang,[1] Qi Zhao,[1] Lianzheng Zheng,[1] Xianggun H. Zheng,[1] Fei N. Zhong,[1] Wenyan Zhong,[1] Xiaojun Zhou,[3] Shiaoping Zhu,[1] Xiaohong Zhu,[1] Hamilton O. Smith,[1] Richard A. Gibbs,[3] Eugene W. Myers,[1] Gerald M. Rubin,[34] J. Craig Venter[1]

Adams et al. (2000)

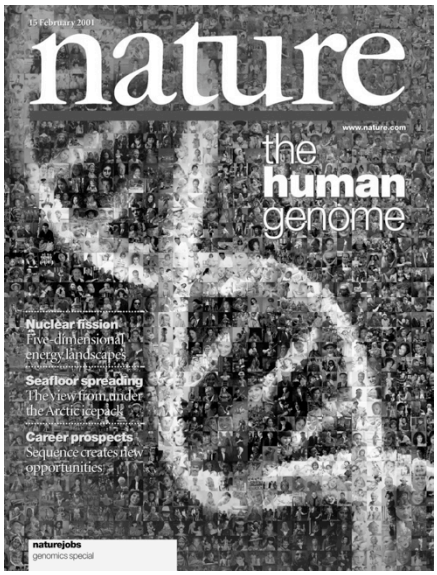
Clone-Based Shotgun Sequencing



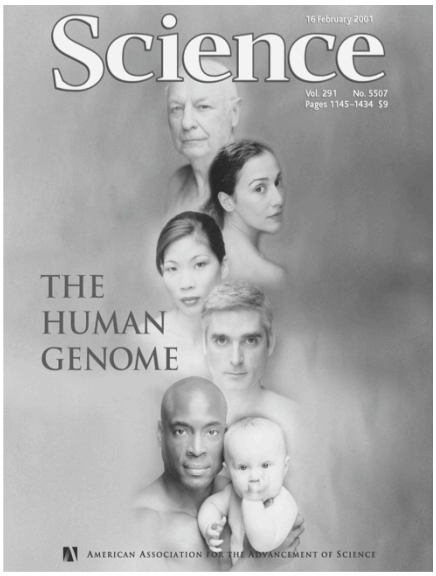
Whole-Genome Shotgun Sequencing



February, 2001 Draft Sequence



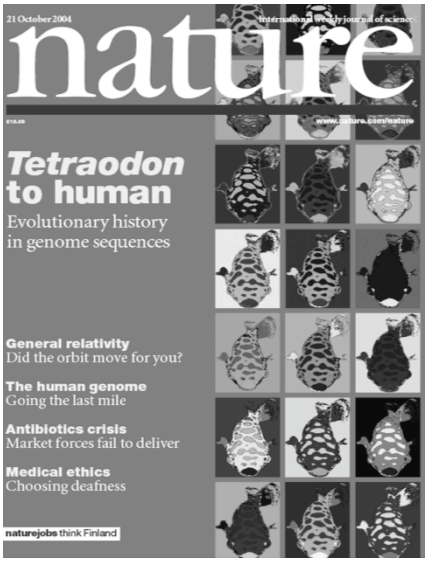
International Human Genome Sequencing Consortium (2001)



Venter et al. (2001)

April, 2003 Completion

October, 2004 Publication



articles

Finishing the euchromatic sequence of the human genome

International Human Genome Sequencing Consortium*

*A list of authors and their affiliations appears in the Supplementary Information

The sequence of the human genome encodes the genetic instructions for human physiology, as well as rich information about human evolution. In 2001, the International Human Genome Sequencing Consortium reported a draft sequence of the euchromatic portion of the human genome. Since then, the international collaboration has worked to convert this draft into a genome sequence with high accuracy and nearly complete coverage. Here, we report the result of this finishing process. The current genome sequence (Build 35) contains 2.85 billion nucleotides interrupted by only 341 gaps. It covers ~99% of the euchromatic genome and is accurate to an error rate of ~1 event per 100,000 bases. Many of the remaining euchromatic gaps are associated with segmental duplications and will require focused work with new methods. The near-complete sequence, the first for a vertebrate, greatly improves the precision of biological analyses of the human genome including studies of gene number, birth and death. Notably, the human genome seems to encode only 20,000–25,000 protein-coding genes. The genome sequence reported here should serve as a firm foundation for biomedical research in the decades ahead.

The Human Genome Project (HGP) was launched in 1990 with the goal of obtaining a highly accurate sequence of the vast majority of the euchromatic portion of the human genome. The initial work followed a two-pronged approach: (1) the mapping of the human and mouse genomes[1–6] to allow the study of inherited disease and provide a crucial scaffold for genome assembly; and (2) the sequencing of organisms with smaller, simpler genomes[7–9] to serve as a testbed for method development and assist in interpreting the human genome. With success along both paths, the sequencing of the human genome itself eventually became feasible. The International Human Genome Sequencing Consortium (IHGSC), an open collaboration involving twenty centres in six countries, was formed to carry out this component of the HGP.

In February 2001, the IHGSC[10] and Celera Genomics* each reported draft sequences providing a first overall view of the human genome. These sequences allowed systematic study of the human genome itself, including identification of genes, combinatorial architecture of proteins, regional differences in genome composition, distribution and history of transposable elements, distribution of polymorphism and relationship between genetic recombination and physical distance. Moreover, systematic knowledge of the human genome has enabled new tools and approaches that have markedly accelerated biomedical research.

Both draft sequences, however, had important shortcomings. The IHGSC sequence, for example, omitted ~10% of the euchromatic genome; it was interrupted by ~150,000 gaps and the order and orientation of many segments within local regions had not been established. The IHGSC thus turned to the challenge of completing the sequence of the euchromatic genome. Operationally, a finished sequence was defined as having an error rate of, at most, one event per 10^4 bases, and the goal for completion was coverage in finished sequence of at least 95% of the euchromatic genome, with the only gaps being those refractory to all available techniques[11] (see http://www.genome.gov/10000923). The goal was challenging because the human genome is replete with such features as dispersed repeats and large segmental duplications, which greatly complicate the determination of genome structure and sequence. In fact, near-complete sequences have been obtained so far only for three multicellular organisms: the nematode[12], mustard weed[13] and the fruitfly[14]. These genomes are all roughly 30-fold smaller than the human genome and have much simpler structure.

We describe here the results of a multiyear effort by the IHGSC towards the goal of a complete human sequence. The number of gaps has been reduced 400-fold to only 341, most of which are associated with segmental duplications and will require new methods for resolution. The assembled near-complete genome sequence has an error rate of only ~1 event per 100,000 bases; it contains 2.85 billion nucleotides and covers ~99% of the euchromatic genome. This paper describes the current genome sequence and the process used to produce it; examines the accuracy and completeness of the sequence; and illustrates biological analyses made possible by the sequence. We do not attempt here a comprehensive analysis of the contents of the human genome. An initial analysis was previously reported[15] and a series of papers is being written describing the individual chromosomes[16–39], including annotation of genes and other features.

Current genome sequence

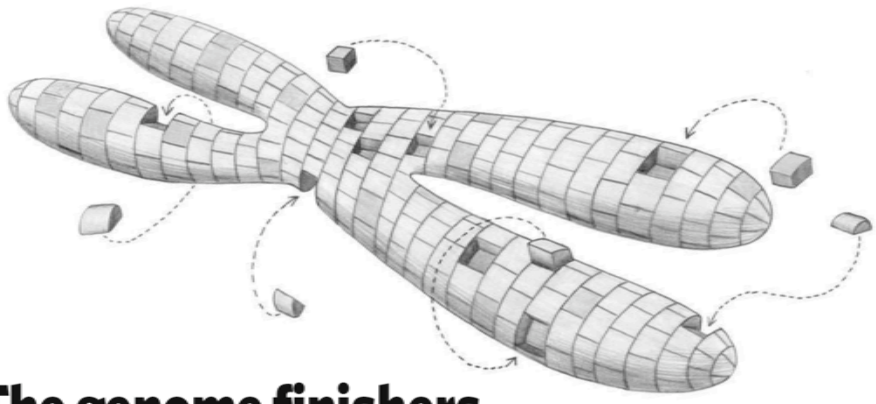
Finishing process

The process of converting the initial draft sequence into a near-complete sequence is referred to as 'finishing'. It is a complex iterative process that proceeds simultaneously at multiple scales, ranging from single nucleotides to the integrity of whole chromosomes. The fundamental challenge is that genomic regions that are not well represented or readily resolved through random shotgun sequencing tend to be highly enriched in problematic sequences. Resolving such regions required the development of special approaches, which evolved substantially over time and varied among centres.

Broadly, the finishing process involved two distinct components: (1) producing finished maps, consisting of continuous and accurate paths of overlapping large-insert clones spanning the euchromatic region of each chromosome arm; and (2) producing finished clones, consisting of continuous and accurate nucleotide sequence across each large-insert clone. In practice, these two components were tightly intertwined in that progress in each often depended on results from the other. The components are described in Boxes 1 and 2. Further information about the finishing process and finishing standards can be found in the Supplementary Information (Note 1) and at http://www.genome.gov/10000923.

In total, we generated a shotgun sequence from 59,208 large-insert clones (total length ~5.84 gigabases (Gb)) and finished the sequence from 45,742 of these clones (total length ~3.67 Gb). The clones consisted primarily of bacterial artificial chromosomes

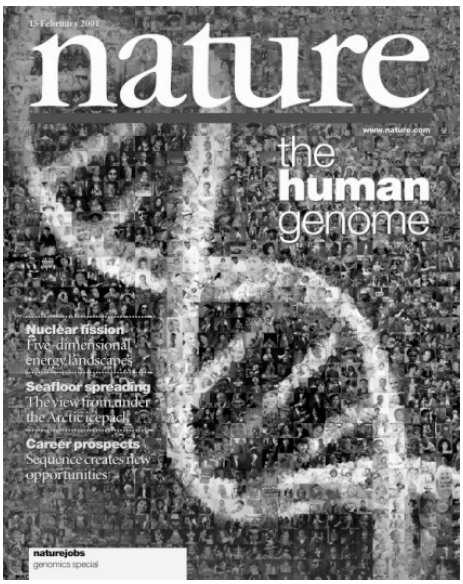
International Human Genome Sequencing Consortium (2004)



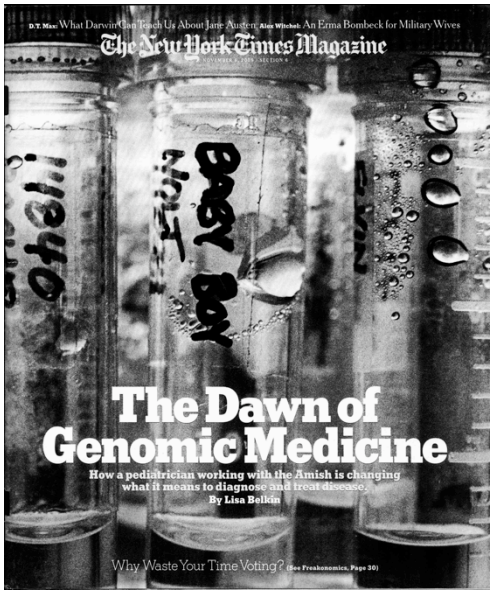
The genome finishers

Dedicated scientists are working hard to close the gaps, fix the errors and finally complete the human genome sequence. **Elie Dolgin** looks at how close they are.

***Nature* (2009)**



Human Genome Project



The Path to Genomic Medicine

HGP

Realization of Genomic Medicine

Genomic Medicine

Healthcare tailored to the individual based on genomic information

The Path to Genomic Medicine

HGP

Realization of Genomic Medicine

✓ *"Fulfilling the Promise"*

?

Mapping the Human Genome	**~1990 to ~2000**	**The Human Genome Project**
Sequencing the Human Genome	**~1998 to ~2003**	
Interpreting the Human Genome Sequence	**~2003 to ???**	***Beyond*** **The Human Genome Project**

~3,000 bp (0.0001%) of Human Genome Sequence

TGCCGCGGAACTTTTCGGCTCTCTAAGGCTGTATTTTGATATACGAAAGGCACATTTTCCTTCCCTTTTCAAAATGCACCTTGCAAACGTAACAG
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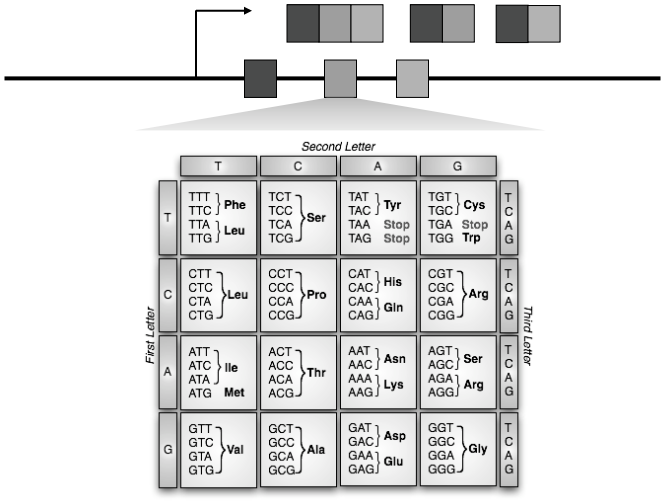
Coding Sequences (i.e., Genes)



The Genetic Code

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TGCCGCGGAACTTTTCGGCTCTCTAAGGCTGTATTTTGATATACGAAAGGCACATTTTCCTTCCCTTTTCAAAATGCACCTTGCAAACGTAACAG
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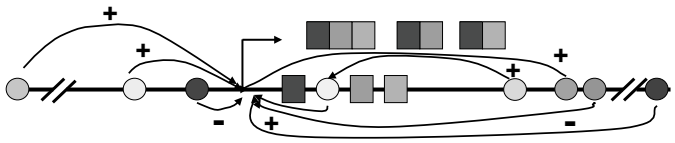
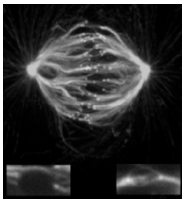
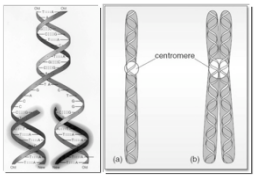
Non-Coding Functional Sequences



Gene Regulation





?

Chromosome Packaging | Chromosome Segregation | Chromosome Replication | Non-Coding RNAs

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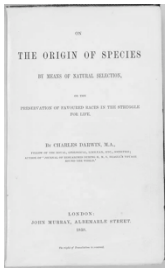
- Corresponds to ~18-22K Genes
- Many More than ~22K Different Proteins
- Good Inventory at Present

~3.5% Functional But Non-Coding

- Gene Regulatory Elements
- Chromosomal Functional Elements
- Undiscovered Functional Elements (NOT Yet in Textbooks!)
- Poor Inventory at Present

Foundational Milestones in Genetics & Genomics



Darwin

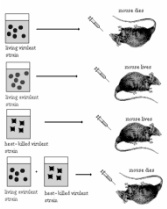
1859

Mendel

1865

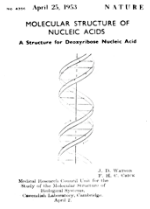
Miescher

1871



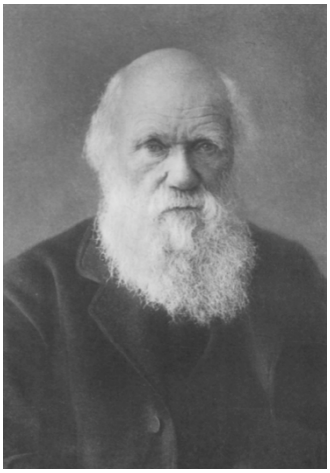
Avery

1944



Watson & Crick

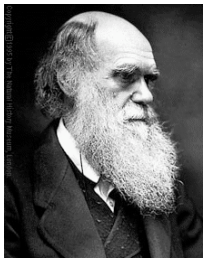
1953



Charles Darwin
Born February 12, 1809

"It is not the strongest of the species that survives, nor the most intelligent that survives. It is the one that is the most adaptable to change."

(Attributed to Darwin)

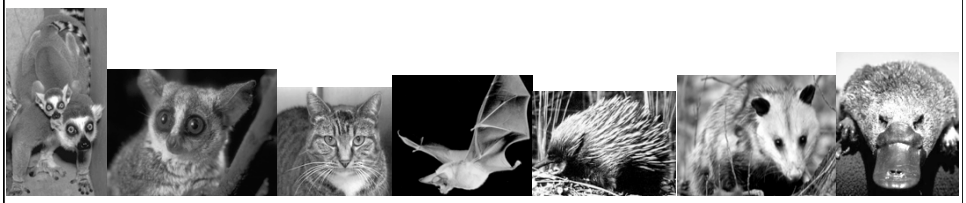


Charles Darwin (1809-1882)

"For the last three and a half billion years, evolution has been taking notes."

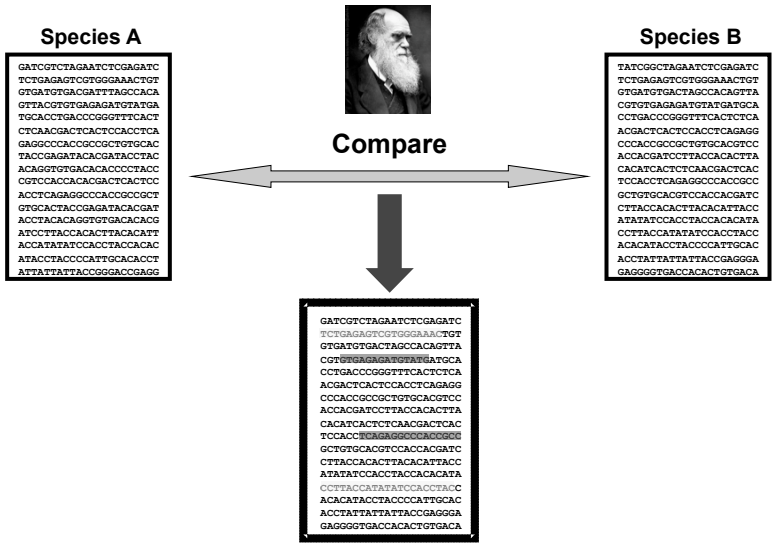
–Eric Lander

Inter-Species Sequence Comparisons



Comparative Sequence Analysis

Using the 'Experiments of Evolution' to Decode the Human Genome



Sequences in Common (i.e., 'Conserved' or 'Constrained')

Vertebrate Genome Sequences

Mouse

Rat

Chicken

Chimpanzee

Dog

Macaque

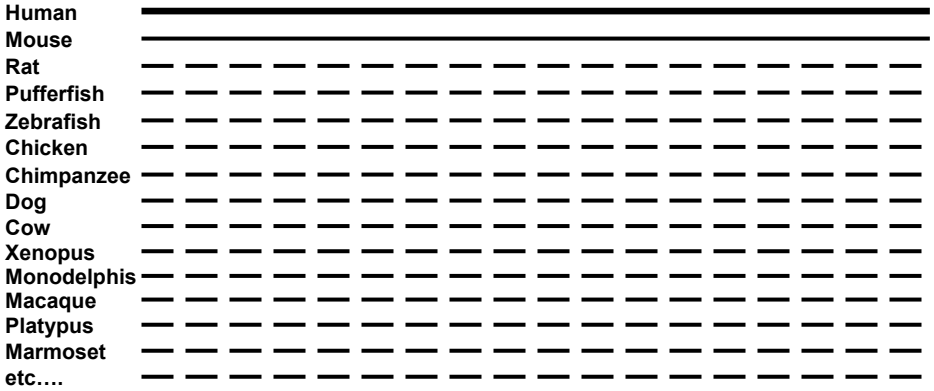
Monodelphis

Platypus

Cow

Pufferfish

Diverse Landscape of Genome Sequencing

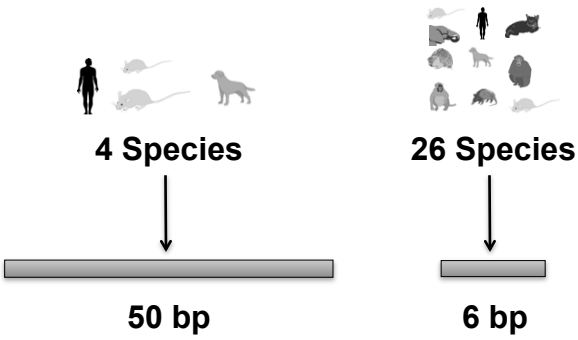


More Species = More Power

A Model of the Statistical Power
of Comparative Genome Sequence Analysis

Sean R. Eddy

***PLoS Biology* (2005)**

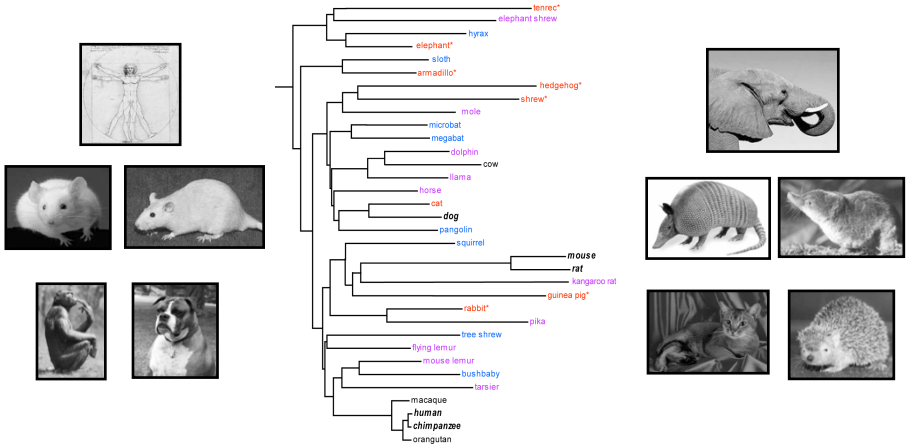


'Light Sampling' of Many Mammalian Genomes

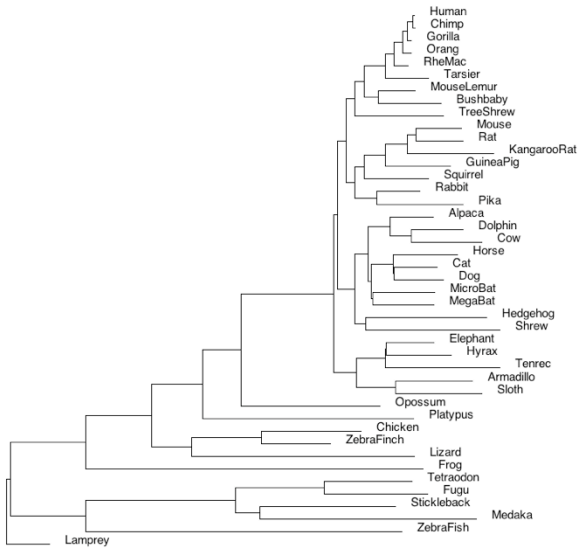
An initial strategy for the systematic identification of functional elements in the human genome by low-redundancy comparative sequencing

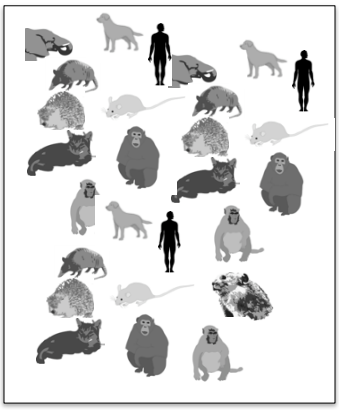
Elliott H. Margulies*†, Jade Vinson†‡, NISC Comparative Sequencing Program*§¶, Webb Miller||, David B. Jaffe‡, Kerstin Lindblad-Toh‡, Jean Chang‡, Eric D. Green*§, Eric S. Lander‡, James C. Mullikin*§**, and Michele Clamp†**

***PNAS* (2005)**

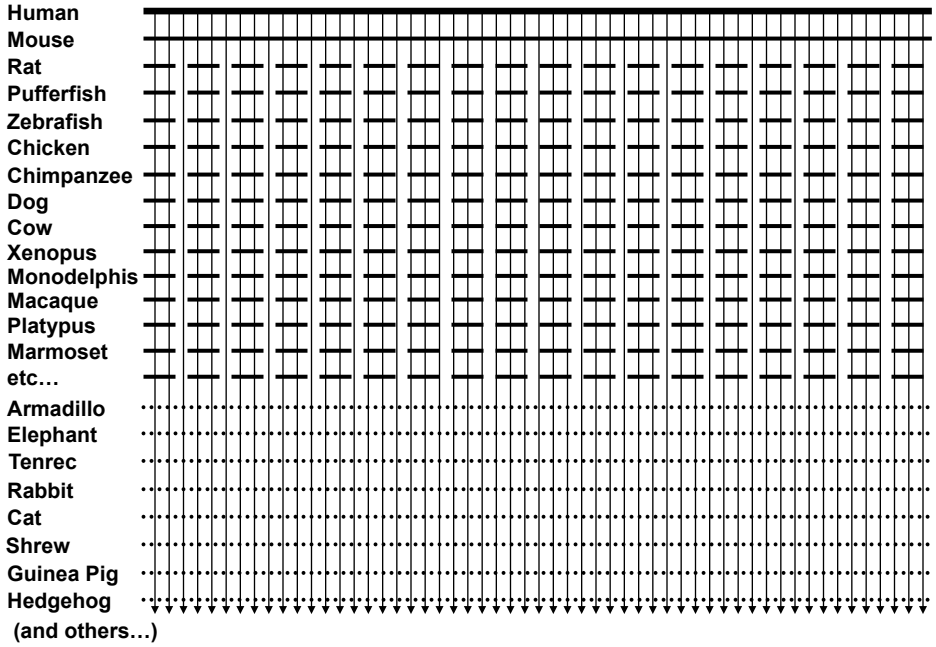


22 Additional Mammalian Genome Sequences (@ Low Redundancy)

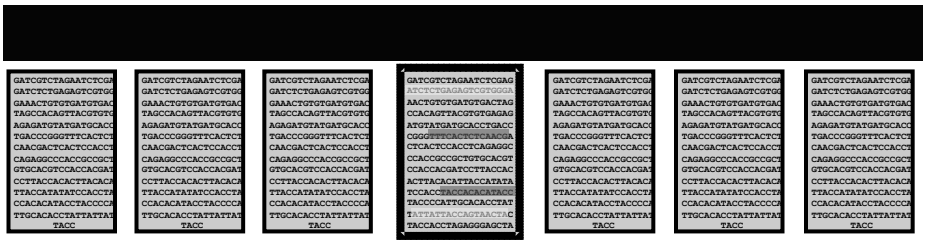




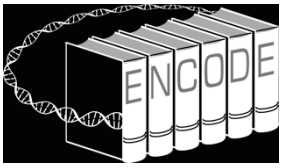
Diverse Landscape of Genome Sequencing



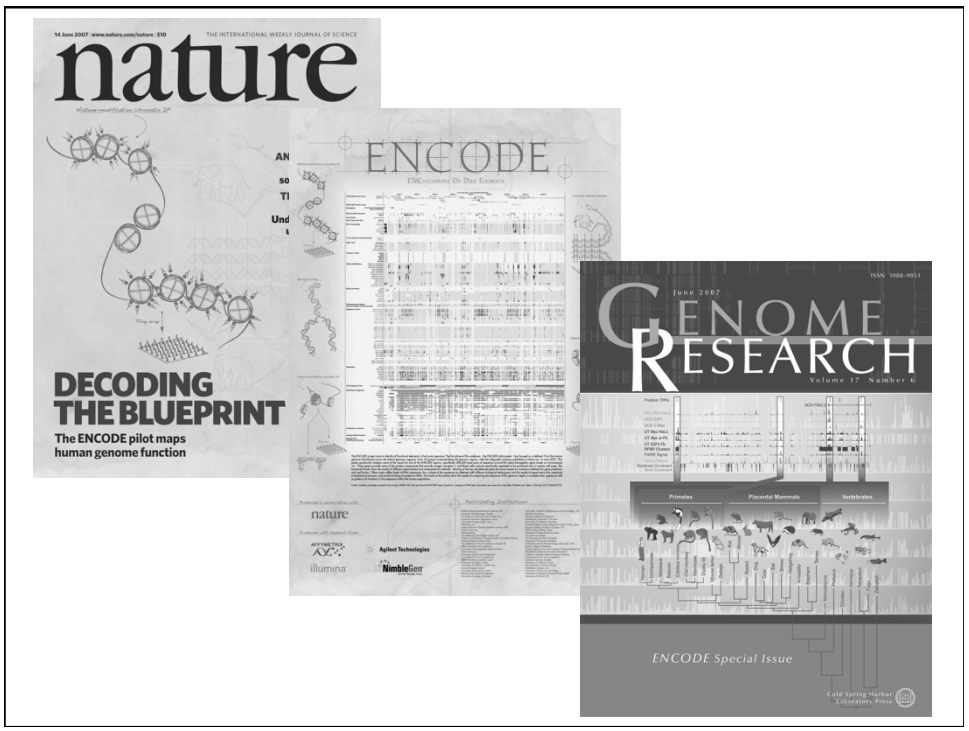
Multi-Species Sequence Comparisons



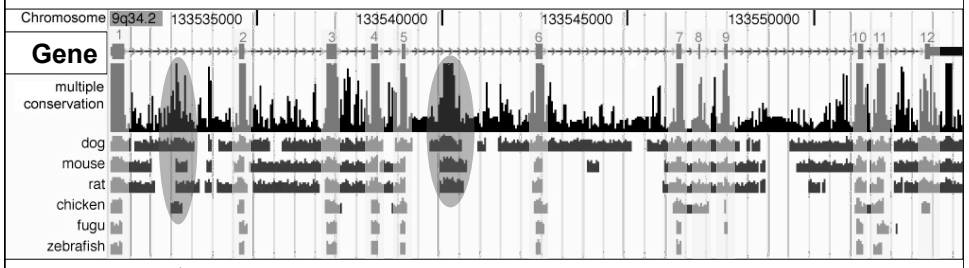
ENCODE Project



- ENCODE: ENCyclopedia Of DNA Elements
- Goal: Compile a *Comprehensive Encyclopedia* of All Functional Elements in the Human Genome
- Initial Pilot Project: 1% of Human Genome
- Apply Multiple, Diverse Approaches to Study and Analyze that 1% in a Consortium Fashion

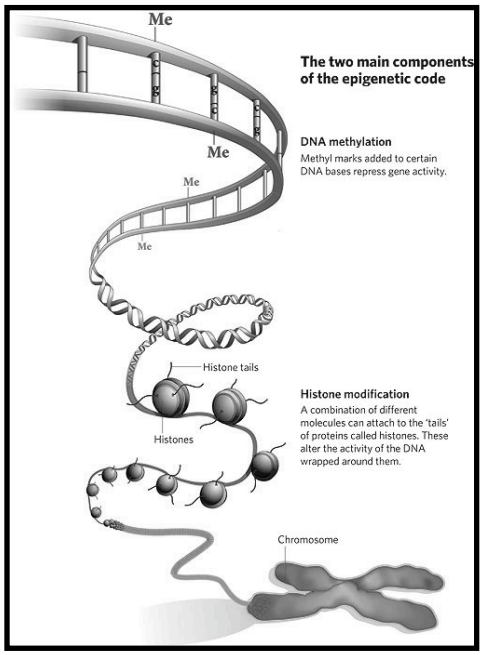


Conserved Coding and Non-Coding Sequences



Augment with 'Functional Annotations'

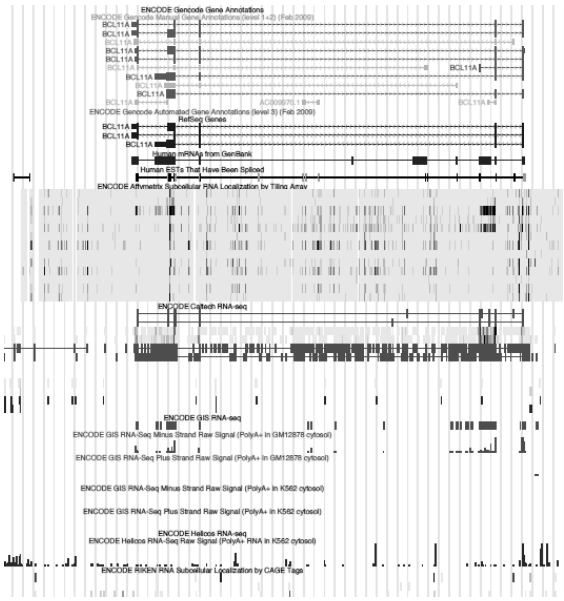
The Epigenetic Landscape

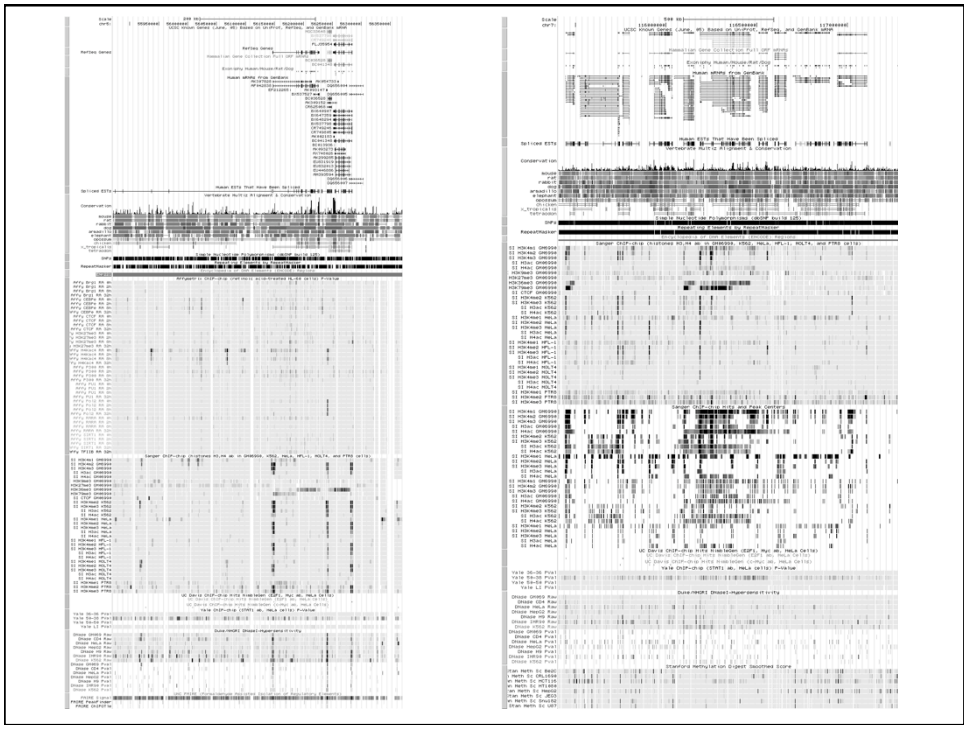


ENCODE: Lots of Data and Data Types

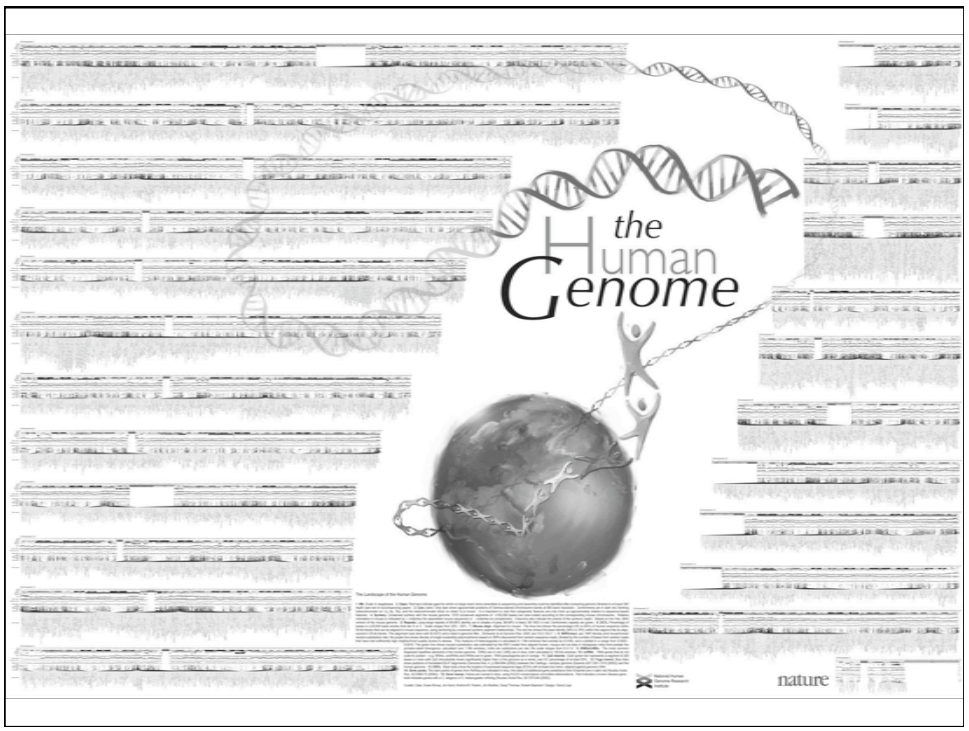
Generated by:

RNA-Seq
RNA-array
TF ChIP-Seq
Histone modif ChIP-Seq
DNaseHS-Seq
FAIRE-Seq
Methyl-Seq
Methyl27-bisulfite
etc.
etc.
etc.

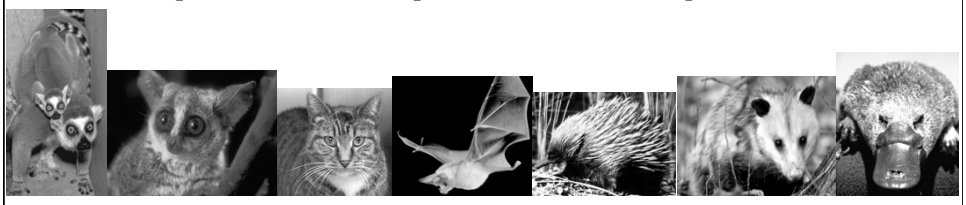




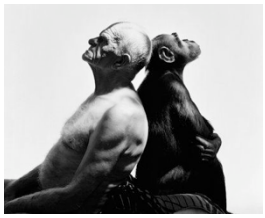
Expanding ENCODE Portfolio

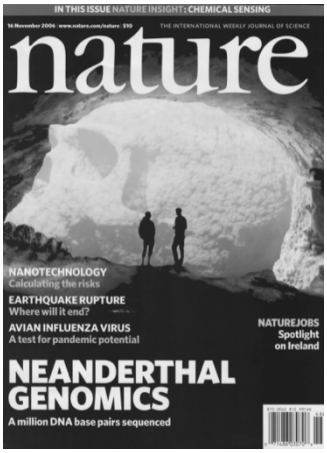


Inter-Species Sequence Comparisons



The Genomics of Human Evolution





GENOME 10K©

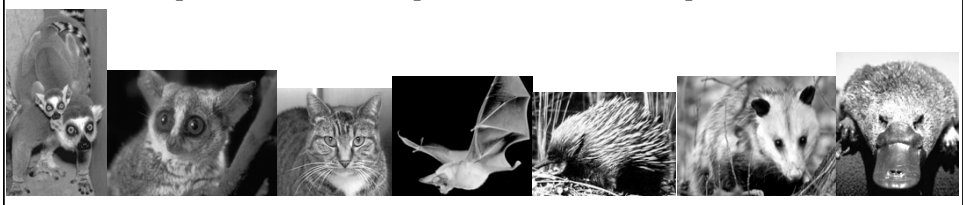
(David Haussler, Stephen O'Brien, & Oliver Ryder)

Genome 10K: A Proposal to Obtain Whole-Genome Sequence for 10 000 Vertebrate Species

GENOME 10K COMMUNITY OF SCIENTISTS*

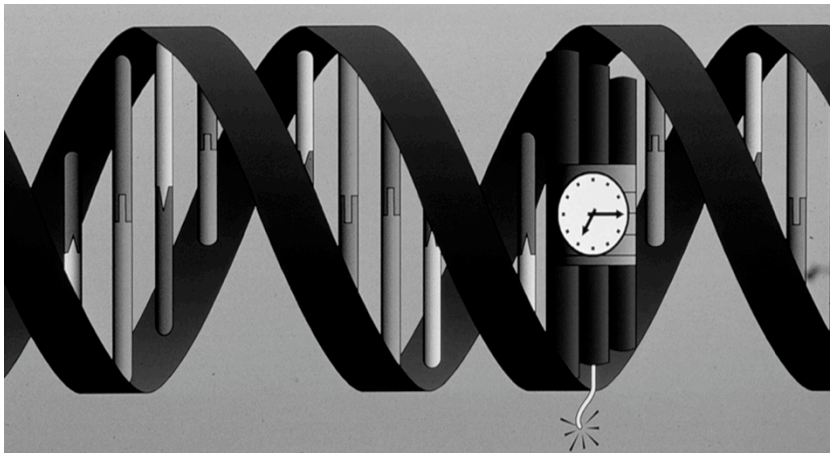
***J. Heredity* (2009)**

Inter-Species Sequence Comparisons

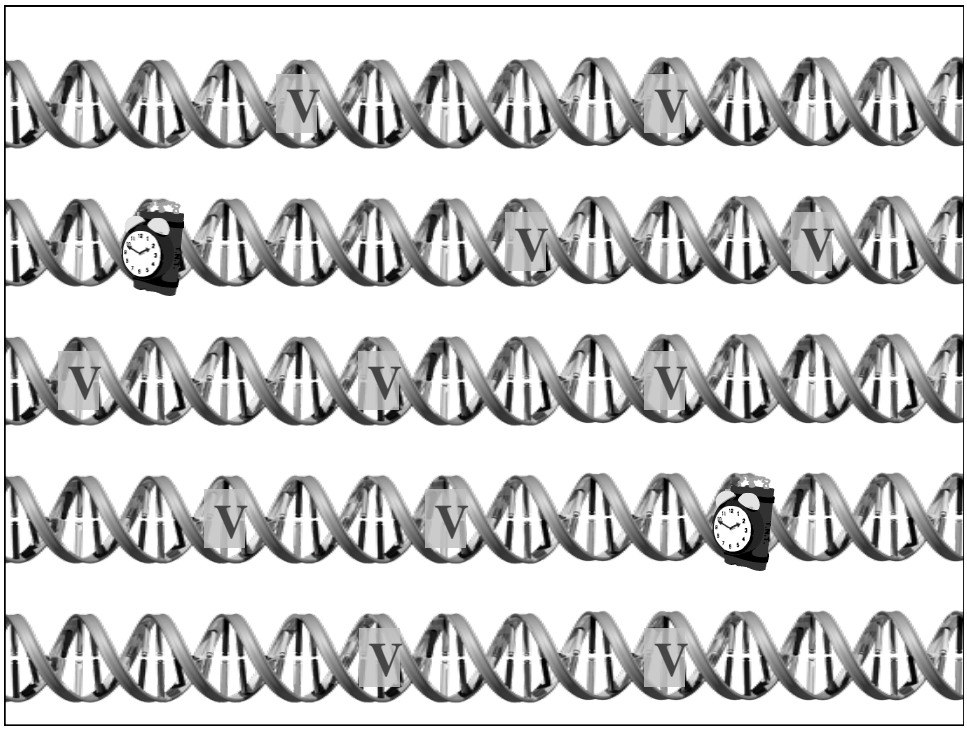


Intra-Species Sequence Comparisons

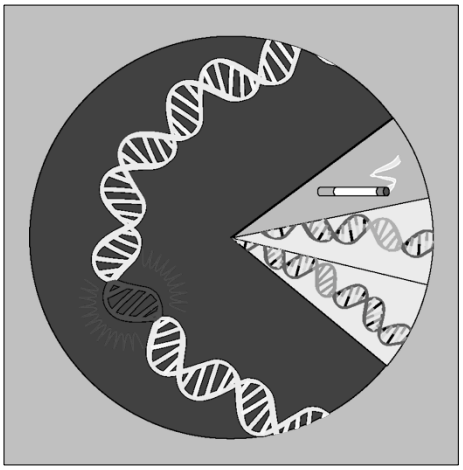
All humans are ~99.7% identical at the DNA sequence level, and yet…



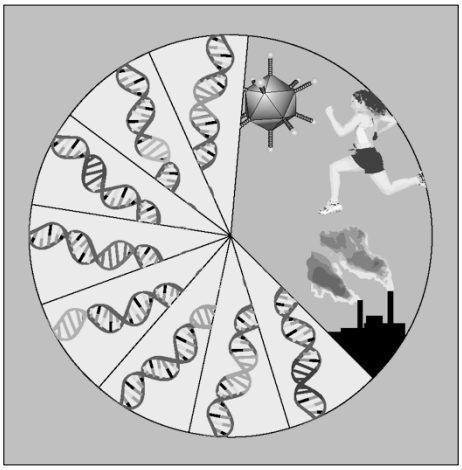
all of us carry a significant number of 'glitches' in our genomes.



Genomic Architecture of Genetic Diseases

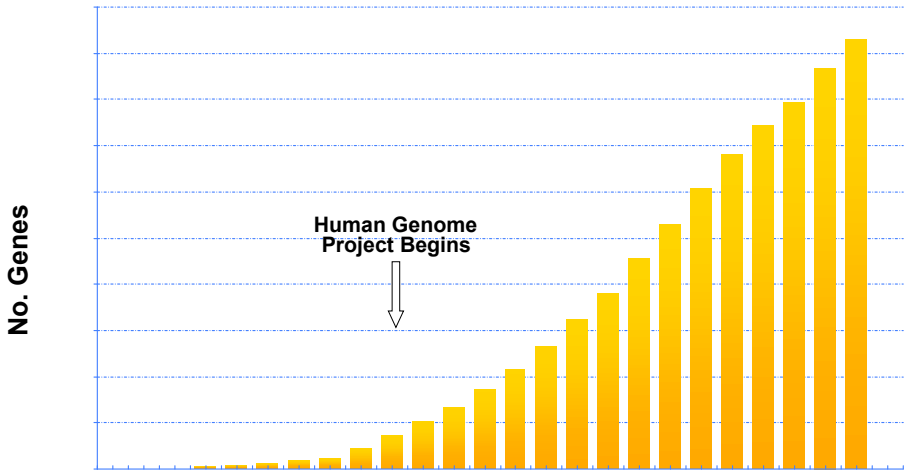


Rare, Simple, Monogenic, Mendelian…



Common, Complex, Multigenic, Non-Mendelian…

Human Disease Genes Identified: 1981-2005

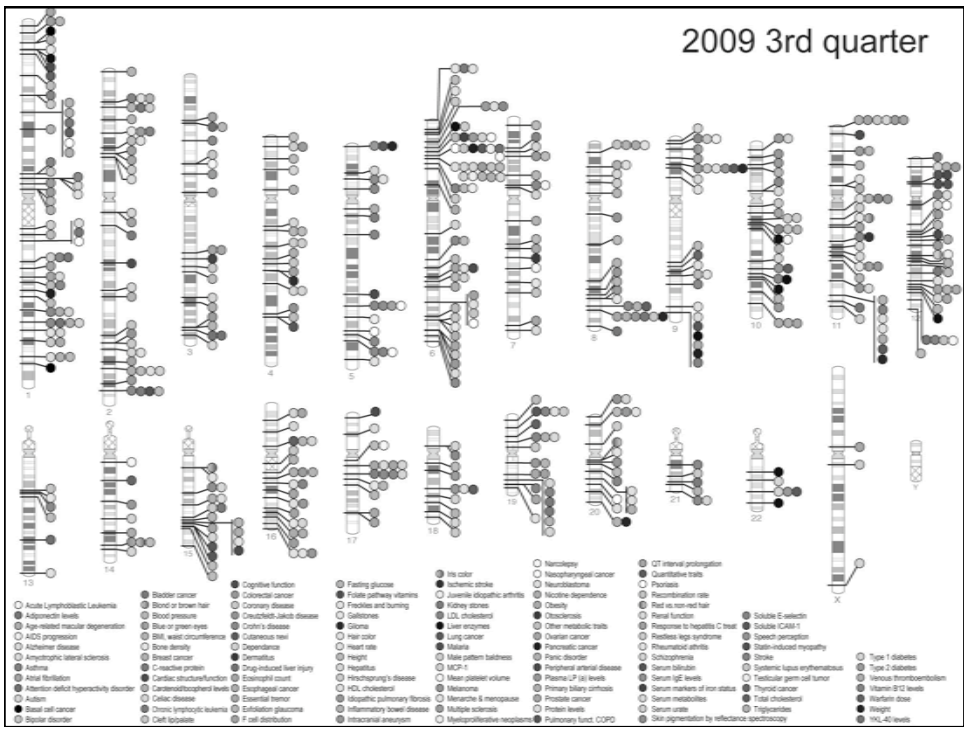


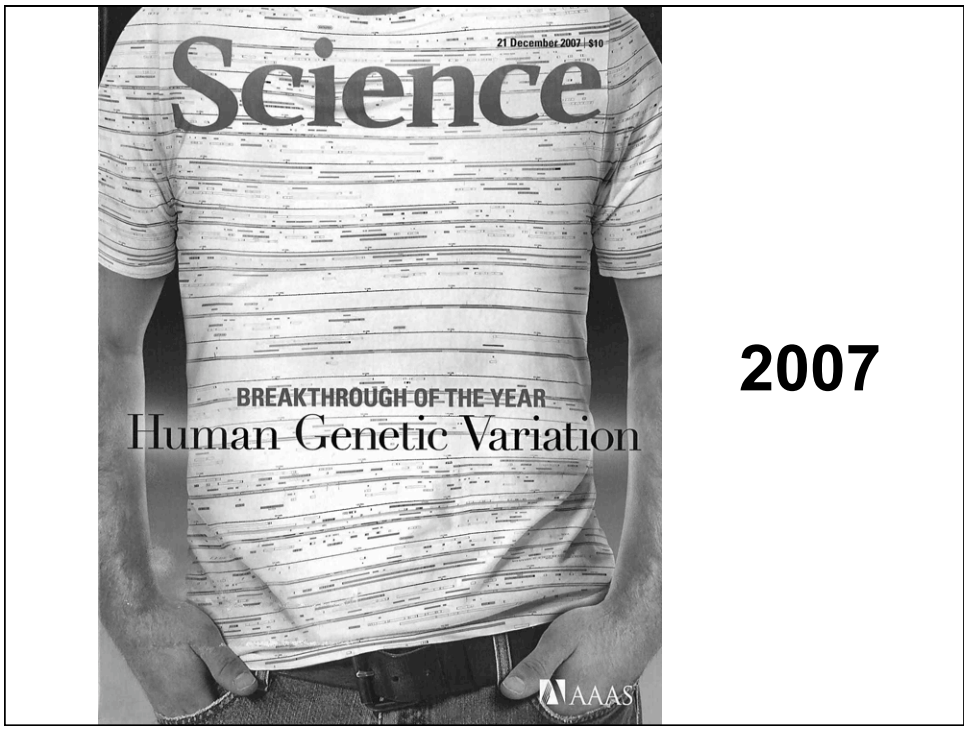
Source: Online Mendelian Inheritance in Man

The First HapMap Success Story: Age-Related Macular Degeneration

Complement Factor H Polymorphism in Age-Related Macular Degeneration

Robert J. Klein,[1] Caroline Zeiss,[2*] Emily Y. Chew,[3*] Jen-Yue Tsai,[4*] Richard S. Sackler,[1] Chad Haynes,[1] Alice K. Henning,[5] John Paul SanGiovanni,[3] Shrikant M. Mane,[6] Susan T. Mayne,[7] Michael B. Bracken,[7] Frederick L. Ferris,[3] Jurg Ott,[1] Colin Barnstable,[2] Josephine Hoh[7†]


2009 3rd quarter


Science
21 December 2007 | $10
BREAKTHROUGH OF THE YEAR
Human Genetic Variation
AAAS

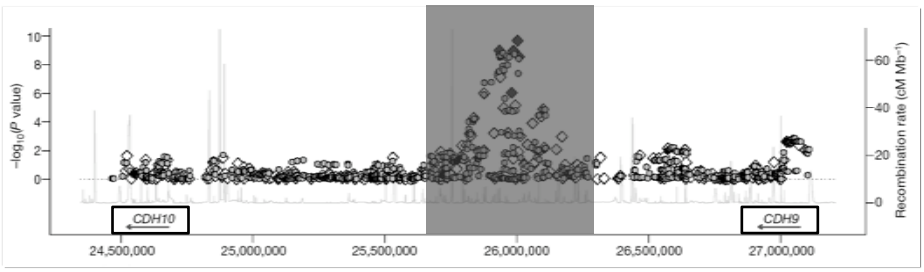
2007

Genetic Association within Intergenic Region

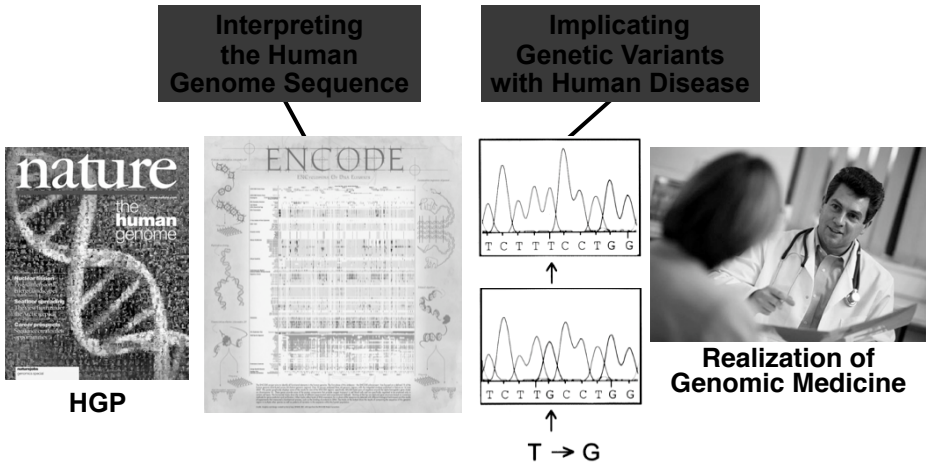
Common genetic variants on 5p14.1 associate with autism spectrum disorders

Kai Wang[1]*, Haitao Zhang[1]*, Deqiong Ma[2]*, Maja Bucan[3], Joseph T. Glessner[1], Brett S. Abrahams[4], Daria Salyakina[2], Marcin Imielinski[1], Jonathan P. Bradfield[1], Patrick M. A. Sleiman[1], Cecilia E. Kim[1], Cuiping Hou[1], Edward Frackelton[1], Rosetta Chiavacci[1], Nagahide Takahashi[5], Takeshi Sakurai[5], Eric Rappaport[6], Clara M. Lajonchere[7], Jeffrey Munson[8], Annette Estes[9], Olena Korvatska[8], Joseph Piven[9], Lisa I. Sonnenblick[4], Ana I. Alvarez Retuerto[4], Edward I. Herman[4], Hongmei Dong[4], Ted Hutman[4], Marian Sigman[4], Sally Ozonoff[10], Ami Klin[11], Thomas Owley[12], John A. Sweeney[12], Camille W. Brune[12], Rita M. Cantor[13], Raphael Bernier[8], John R. Gilbert[2], Michael L. Cuccaro[2], William M. McMahon[14], Judith Miller[14], Matthew W. State[11], Thomas H. Wassink[15], Hilary Coon[14], Susan E. Levy[6], Robert T. Schultz[6], John I. Nurnberger Jr[16], Jonathan L. Haines[17], James S. Sutcliffe[18], Edwin H. Cook[12], Nancy J. Minshew[19], Joseph D. Buxbaum[5,20], Geraldine Dawson[8], Struan F. A. Grant[1,6], Daniel H. Geschwind[4], Margaret A. Pericak-Vance[2], Gerard D. Schellenberg[21] & Hakon Hakonarson[1,6]

***Nature* (2009)**

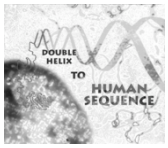


The Pathway to Genomic Medicine



Human Genome Sequence

>$1,000,000,000

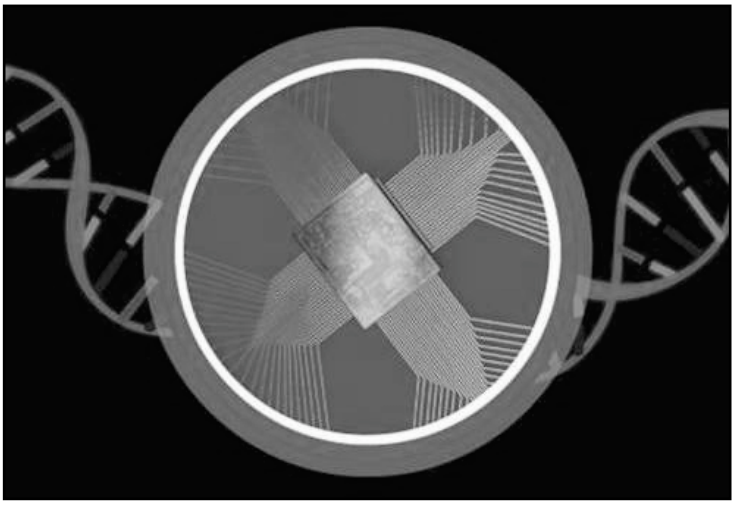


↓

↓

↓

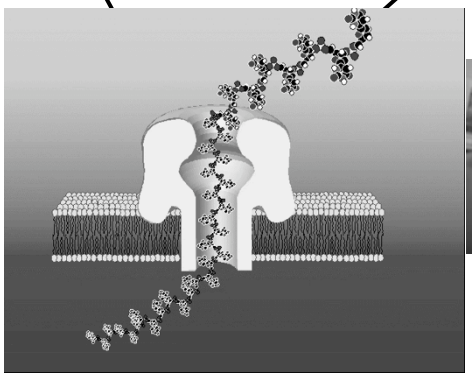
~$1,000



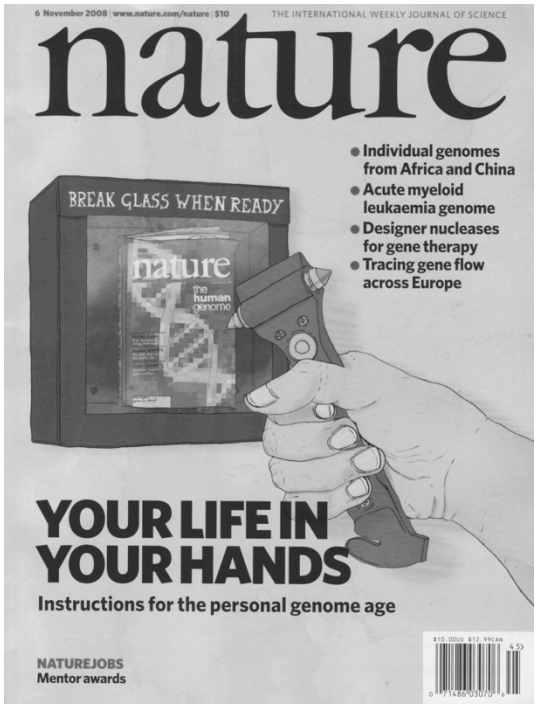
The Path to Genomic Medicine

Interpreting the Human Genome Sequence

Implicating Genetic Variants with Human Disease



Realization of Genomic Medicine

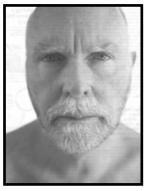


Individual Genome Sequences

The Diploid Genome Sequence of an Individual Human

Samuel Levy[1*], Granger Sutton[1], Pauline C. Ng[1], Lars Feuk[2], Aaron L. Halpern[1], Brian P. Walenz[1], Nelson Axelrod[1], Jiaqi Huang[1], Ewen F. Kirkness[1], Gennady Denisov[1], Yuan Lin[1], Jeffrey R. MacDonald[2], Andy Wing Chun Pang[2], Mary Shago[2], Timothy B. Stockwell[1], Alexia Tsiamouri[1], Vineet Bafna[3], Vikas Bansal[3], Saul A. Kravitz[1], Dana A. Busam[1], Karen Y. Beeson[1], Tina C. McIntosh[1], Karin A. Remington[1], Josep F. Abril[4], John Gill[1], Jon Borman[1], Yu-Hui Rogers[1], Marvin E. Frazier[1], Stephen W. Scherer[2], Robert L. Strausberg[1], J. Craig Venter[1]

***PLoS Biol* (2007)**



The complete genome of an individual by massively parallel DNA sequencing

David A. Wheeler[1]*, Maithreyan Srinivasan[2]*, Michael Egholm[2]*, Yufeng Shen[1]*, Lei Chen[1], Amy McGuire[3], Wen He[2], Yi-Ju Chen[2], Vinod Makhijani[2], G. Thomas Roth[2], Xavier Gomes[2], Karrie Tartaro[2†], Faheem Niazi[2], Cynthia L. Turcotte[2], Gerard P. Irzyk[2], James R. Lupski[3,5,6], Craig Chinault[4], Xing-zhi Song[1], Yue Liu[1], Ye Yuan[1], Lynne Nazareth[1], Xiang Qin[1], Donna M. Muzny[1], Marcel Margulies[2], George M. Weinstock[1,4], Richard A. Gibbs[1,4] & Jonathan M. Rothberg[2†]

***Nature* (2008)**

Accurate whole human genome sequencing using reversible terminator chemistry

A list of authors and their affiliations appears at the end of the paper

***Nature* (2008)**

The diploid genome sequence of an Asian individual

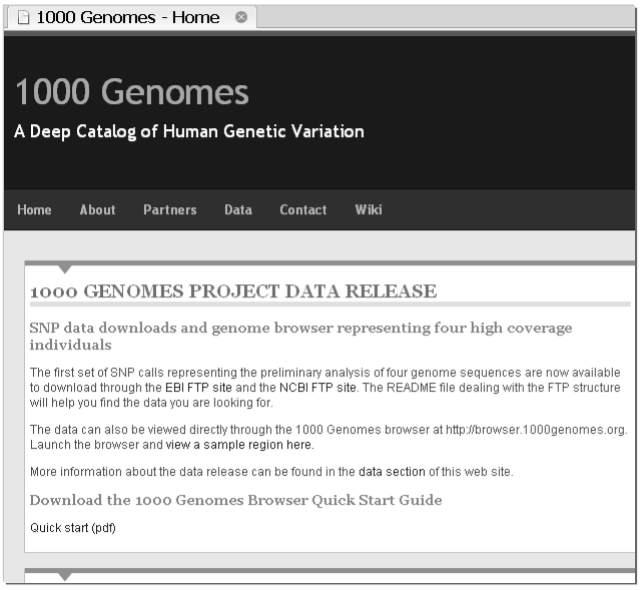
Jun Wang[1,2,3,4]*, Wei Wang[1,3]*, Ruiqiang Li[1,3,4]*, Yingrui Li[1,3,4]*, Geng Tian[1,2], Laurie Goodman[1], Wei Fan[1], Junqing Zhang[1], Jun Li[1], Juanbin Zhang[1], Yiran Guo[1,2], Binxiao Feng[1], Heng Li[1,5], Yao Lu[1], Xiaodong Fang[1], Huiqing Liang[1], Zhenglin Du[1], Dong Li[1], Yiqing Zhao[1,2], Yujie Hu[1,2], Zhenzhen Yang[1], Hancheng Zheng[1], Ines Hellmann[6], Michael Inouye[6], John Pool[6], Xin Yi[1,2], Jing Zhao[1], Jinjie Duan[1], Yan Zhou[1], Junjie Qin[1,2], Lijia Ma[1,2], Guoqing Li[1], Zhentao Yang[1], Guojie Zhang[1,2], Bin Yang[1], Chang Yu[1], Fang Liang[1,2], Wenjie Li[1], Shaochuan Li[1], Dawei Li[1], Peixiang Ni[1], Jue Ruan[1,2], Qibin Li[1,2], Hongmei Zhu[1], Dongyuan Liu[1], Zhike Lu[1], Ning Li[1,2], Guangwu Guo[1,2], Jianguo Zhang[1], Jia Ye[1], Lin Fang[1], Qin Hao[1,2], Quan Chen[1,2], Yu Liang[1,2], Yeyang Su[1,2], A. san[1,2], Cuo Ping[1,2], Shuang Yang[1], Fang Chen[1,2], Li Li[1], Ke Zhou[1], Hongkun Zheng[1,4], Yuanyuan Ren[1], Ling Yang[1], Yang Gao[1,6], Guohua Yang[1,2], Zhuo Li[1], Xiaoli Feng[1], Karsten Kristiansen[6], Gane Ka-Shu Wong[1,2,10], Rasmus Nielsen[7], Richard Durbin[8], Lars Bolund[1,11], Xiuqing Zhang[1,6], Songgang Li[1,2,3] & Huanming Yang[1,2,3] & Jian Wang[1,2,3]

***Nature* (2008)**

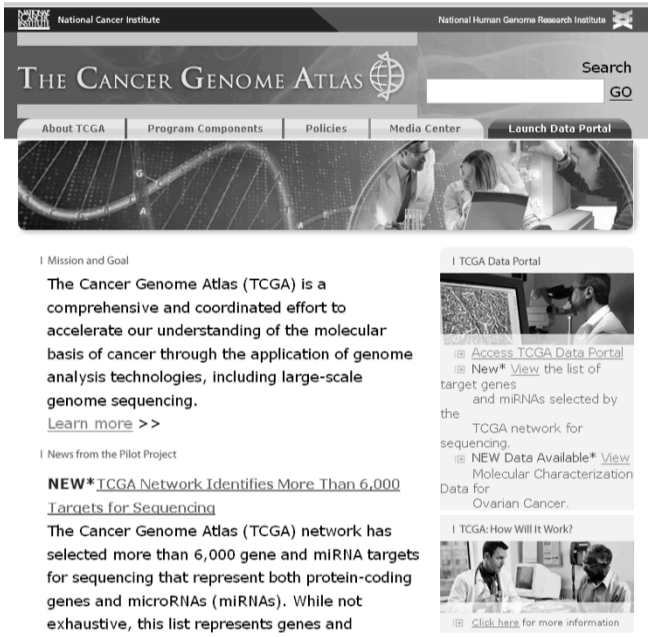
A highly annotated whole-genome sequence of a Korean individual

Jong-Il Kim[1,2,4,5]*, Young Seok Ju[1,2]*, Hansoo Park[1,3], Sheehyun Kim[4], Seonwook Lee[4], Jae-Hyuk Yi[1], Joann Mudge[6], Neil A. Miller[6], Dongwan Hong[1], Callum J. Bell[6], Hye-Sun Kim[4], In-Soon Chung[4], Woo-Chung Lee[4], Ji-Sun Lee[4], Seung-Hyun Seo[7], Ji-Young Yun[5], Hyun Nyun Woo[4], Heewook Lee[4], Dongwhan Suh[1,2,3], Seungbok Lee[1,2,3], Hyun-Jin Kim[1,3], Maryam Yavartanoo[1,2], Minhye Kwak[1,2], Ying Zheng[1,2], Mi Kyeong Lee[1], Hyunjun Park[1], Jeong Yeon Kim[1], Omer Gokcumen[7], Ryan E. Mills[7], Alexander Wait Zaranek[6], Joseph Thakuria[6], Xiaodi Wu[6], Ryan W. Kim[6], Jim J. Huntley[6], Shujun Luo[6], Gary P. Schroth[6], Thomas D. Wu[6], HyeRan Kim[4], Kap-Seok Yang[4], Woong-Yang Park[1,2,5], Hyungtae Kim[4], George M. Church[9], Charles Lee[7], Stephen F. Kingsmore[6] & Jeong-Sun Seo[1,2,3,4,5]

***Nature* (2009)**

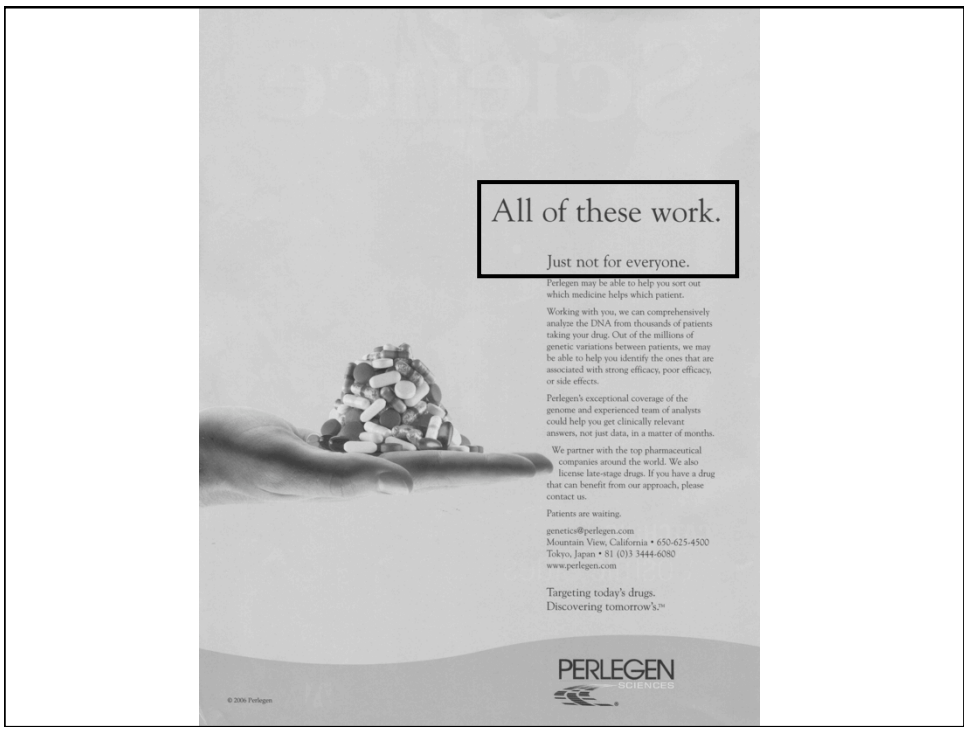


1000genomes.org

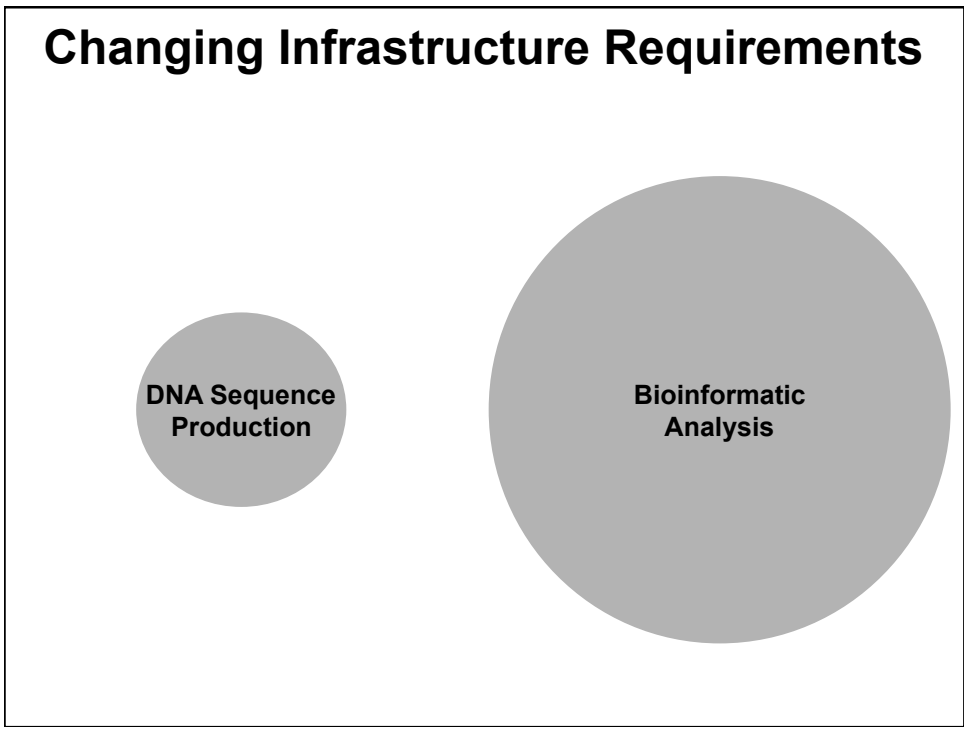


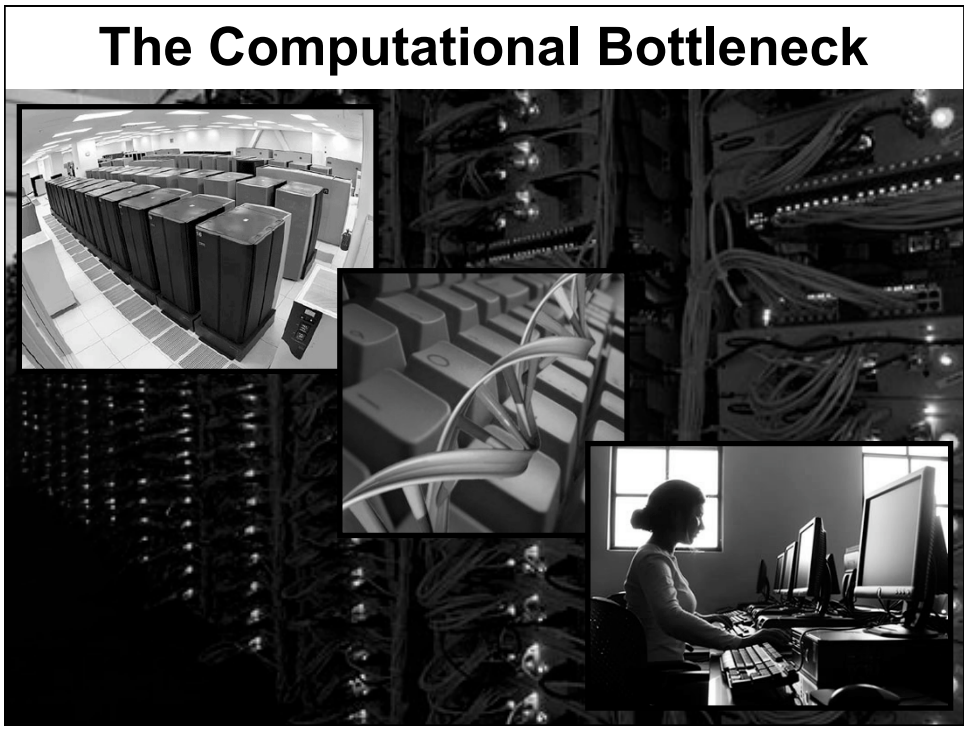
cancergenome.nih.gov

nihroadmap.nih.gov/hmp

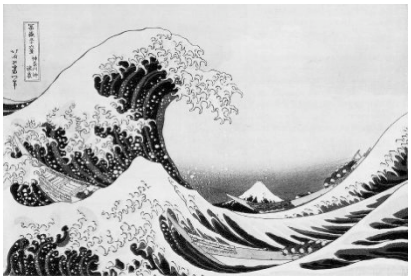


Realities of New DNA Sequencing Technologies…


Changing Infrastructure Requirements
DNA Sequence Production
Bioinformatic Analysis


The Computational Bottleneck

The Genomic Era: *circa* 2010



The Genomic Revolution Continues

The Top 10 Medical Advances of the Decade

By PEGGY PECK and LAUREN COX
ABC News Medical Unit in Collaboration with MedPage Today
Dec. 17, 2009

ABC NEWS
6 comments

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The first decade of the 21st century brought a number of discoveries, mistakes and medical advances that influenced medicine from the patient's bedside to the medicine cabinet.

Dr. John Sulston, Director of the Sanger Centre near Cambridge takes part in the Human Genome Project. (Ho New/Reuters)

In some cases, these advances changed deeply rooted beliefs in medicine. In others, they opened up possibilities beyond what doctors thought was possible years ago.

ABC News, in collaboration with MedPage Today, reached out to more than 800 specialists for their suggestions. More than 125 experts in various fields and specialties responded. Their suggestions were then sent to the American Association for the History of Medicine, which narrowed the pool down to an authoritative list of 10 medical advances this decade that have had the most impact.

1. Human Genome Discoveries Reach the Bedside

In 2000, scientists in California released a rough draft of the human genome to the public on the Internet. For the first time, the world could download and read the complete set of human genetic information and begin to discover what our roughly 23,000 genes do.

Mapping the human genome was a race involving time and money in the 1990s, with two competitors at the lead -- the government-funded Human Genome Project, which completed its task in 15 years using more than $3 billion in taxpayer money, and a private company, Celera Genomics, which used $100 million and took less than a decade.

Both groups announced drafts of the human genome at a June 26, 2000 press conference with then president Bill Clinton and former British Prime Minister Tony Blair.